GENETIC VARIATION IN CENTRAL ASIA: AN EXAMINATION OF POPULATION HISTORY AND STRUCTURE

A Dissertation

by

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ABSTRACT

The population structure of Central Asia and the effects of population history on that structure have not been well studied. To address this gap, 4,169 mtDNA control region sequences from Central Asia and the surrounding areas (Caucasus, East Asia, East Europe, and northern and southern Asia) sourced from GenBank were analyzed. MtDNA sequences were aligned using MAFFT version 7 and haplogroups were assigned with HaploGrep 2.0. Arlequin 3.5.2 was used to calculate the haplotype diversity, nucleotide diversity, and the mean number of pairwise differences, and to perform an AMOVA. Additionally, genetic distances were calculated between all populations and used in PCA to visualize the distribution of genetic diversity. Lastly, the percentages of mtDNA haplogroups in each population were estimated and used in PCA to examine clustering patterns.

The results of this study show that Central Asian populations have a high degree of genetic variation as evidenced by high haplogroup, haplotype, and nucleotide diversities. This genetic variation has been shaped by admixture with populations from East and West Eurasia, and indigenous groups from North and South Asia. Most of the haplogroups in Central Asia have an East or West Eurasian origin, with a small percentage of haplogroups from India. Two haplogroups, D4c and G2a, that may have their origins in Central Asia were also identified. A small, but significant portion of the variation in Central Asia can be accounted for by geographic region. This geographic structure is most consistent with an isolation by distance model. Finally, the history of

population interactions within Central Asia has greatly influenced the distribution of genetic variation there. This includes not only recent interactions resulting from the policies of the Soviet Empire, but also those like the movement of Mongol groups into Central Asia beginning thousands of years ago. This study has situated Central Asia in global models of human variation and has provided a framework with which hypotheses regarding the origin and dispersal of humans, Middle and Late Pleistocene hominin interactions, and the geographic extent of Neandertals can be tested.

DEDICATION

For my husband and son, André and Sanders Ford.

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Thank you to my husband André, without his support I would never have been able to complete this dissertation. He has been there for me throughout the long and arduous process of completing my PhD, whether that be providing moral support, a reality check, or taking care of our son while I spent every waking moment enmeshed in the writing process. There is no one else I would rather have by my side.

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CHAPTER I

INTRODUCTION

Central Asia is an area with a diverse history shaped by cultural and linguistic changes resulting from trade, internal and external migrations, and warfare (Comas et al. 1998; Comas et al. 2004). Often viewed as a crossroads between East (eastern Asia) and West (Europe); Central Asia is a borderland that many have thought of as lacking a unique history (Bowles 1977; Comas et al. 2004; Sellier and Sellier 1993). Despite this misconception, throughout its history Central Asia has been a complex assemblage of cultures, habitats, and peoples (Comas et al. 2004; Frank 1990). It is an area that has played a critical, yet poorly understood, role in human history (Calafell et al. 2000; Comas et al. 1998; Wells et al. 2001).

The question of what constitutes Central Asia is a complicated one (Cummings 2012). Central Asia has been defined in different ways culturally, geographically, historically, and politically (Bregel 1996; Cummings 2012; Levi 2007; Miroshnikov 1992). For the purposes of this project, Central Asia will be considered as the republics of Kazakhstan, Kyrgyzstan, Tajikistan, Turkmenistan, and Uzbekistan. This is a politically based definition of Central Asia and has been chosen to coincide with much of the research done in this region (Comas et al. 1998; Cummings 2012; Heyer et al. 2015; Martinez-Cruz et al. 2010).

Central Asia is a region that has been vastly underrepresented in western scientific research, partly because of limitations placed on western researchers by the

former Soviet government (Goldstein and Beall 1994). Yet, with its vast geographic area and central location, it is a region that has the potential to answer important questions about human history (Frank 1999; Quintana-Murci et al. 2004). Additionally, Central Asia is a region with a complex history; one that can help us to understand the genetic effects of different environments; complex cultural phenomenon; overlapping economies, languages, and ways of life; and the consequences of conquests, expansions, and migrations on human populations (Calafell et al. 2000; Comas et al. 1998; Comas et al. 2004).

Climatically, Central Asia is a land of vast differences. Most of its territory is high-altitude regions or huge cold deserts (Akhmetyev et al. 2005; Comas et al. 1998). Despite these environmental difficulties, Central Asia has been occupied since the Lower Paleolithic, with the oldest site dating to between 800,000 and 900,000 years ago (Glantz 2010). Additionally, there is plenty of evidence of occupation during the Middle Paleolithic, including at Teshik-Tash in Uzbekistan where Neandertal remains have been uncovered (Derevianko et al. 2004; Glantz 2010). Despite this long history of occupation, the role that Central Asia played in early *Homo sapiens* origins and settlement is much less clear (Comas et al. 2004; Derevianko and Markin 1992). Multiple hypotheses have been proposed and include: 1) Central Asia was part of a development phase of early *Homo sapiens*, 2) Central Asia operated as a superhighway in the peopling of Europe and/or eastern Asia, and 3) Central Asia was simply a place where Asian and European factions met after their initial expansion (Bowles 1977; Comas et al. 1998; Quintana-Murci et al. 2004).

The history of Central Asia has been governed by the harsh physical environment, which makes stable human settlements difficult to maintain (Comas et al. 1998; Glantz 2010). This is not to say that there have not been in sedentary societies in this region; in fact, urban settlements in urban oases towns have existed for thousands of years here (Khazanov 1995). Despite this, the steppes have provided a land suitable for a roaming pastoral economy (Comas et al. 1998; 2004). Pastoral economies typically sustain low density populations (Zerjal et al. 2002; Heyer et al. 2009). Thus, Central Asia has been more sensitive to demographic variabilities that result in genetic drift than areas that maintain high density populations. Yet, the lack of geographic barriers toward the West has allowed constant movement of populations from the West into Central Asia as well as the converse (Cavalli-Sforza et al. 1994; Kato 1992; Zerjal et al. 2002).

During the Neolithic, significant economic and technological advances were made in Central Asia without substantial external population influxes. The Silk Road was established in the 2nd century BCE and connected the East to the West for more than 16 centuries, until safer ocean trade routes took its place (Beckwith 2009; Comas et al. 1998; Hiro 2009). During the 3rd and 4th centuries CE, Turkic-speaking groups migrated into Central Asia, eventually taking over the territories that Indo-European peoples had controlled. During the 13th century, the Mongol Empire was created by Genghis Khan. Later, the Chinese and then the Russian empires established their rules over the enormous territory of Central Asia (Bowles 1977; Comas et al. 1998; Grousset 1970; Hiro 2009; Levi 2007).

In the past, biological anthropologists have defined Central Asian populations as having a combination of eastern and western anthropometric traits (Bowles 1977; Ginzburg 1968a; Ginzburg 1968b). The global analysis of classical genetic markers by Cavalli-Sforza et al. (1994) did not expand on the idea that Central Asia is intermediate between Europe and Asia. Current models of global human genetic variation are typically based on genetic variation from Africa, Europe, eastern and southern Asia, and sometimes the Americas, but Central Asia is often times glossed over or, in many cases, ignored completely (e.g., Cavalli-Sforza et al. 1994; Pemberton et al. 2013). With few exceptions (see Heyer et al. 2009; Quintana-Murci et al. 2004; Segurel et al. 2008; Segurel et al. 2012), much of the genetic research that has been done on populations in Central Asia has been highly localized (Cui et al. 2010; Li et al. 2009; Shen et al. 2010; Xu et al. 2008) and/or has not used a broad anthropological perspective (Comas et al. 1998; Jin et al. 1999; Wells et al. 2001; Zerjal et al. 2002). The consensus from the current research is that the genetic variation present within people inhabiting Central Asia is the result of admixture between differentiated populations from Europe and East Asia (Comas et al. 1998; Comas et al. 2004; Karafet et al. 2001; Perez-Lezaun et al. 1999; Wells et al. 2001).

Based on the findings of previous studies and general paucity of research in Central Asia, there is a compelling need for a greater understanding of Central Asian population structure and history as a whole and that is what this study attempts to do. This study uses mitochondrial DNA (mtDNA) sequences from Central Asia (Kazakhstan, Kyrgyzstan, Tajikistan, Turkmenistan, and Uzbekistan) and the

surrounding areas (East Europe, the Near East, the Caucasus, and East, North, and South Asia) to examine genetic variation within Central Asia using a holistic perspective. This study provides a better understanding of the genetic relationships among Central Asian populations as well as surrounding areas. In addition, the current research is a step towards adding Central Asia to the worldwide picture of human genetic variation.

Currently, a framework for understanding the genetic relationships among Central Asian populations is lacking. Therefore, many questions are left unanswered. As such, the current research has three main objectives: 1) to examine the population structure of Central Asia and define the genetic relationships among Central Asian populations; 2) to test whether geographic barriers have been or are currently affecting population interactions in Central Asia; and 3) to examine the effect(s) of population history on the modern-day genetic variation in Central Asia.

Q1: How is genetic variation patterned in Central Asia?

Thus far, the genetic research that has been done in Central Asia has demonstrated that Central Asian populations exhibit a high degree of genetic diversity (Chaix et al. 2008; Comas et al. 1998; Comas et al. 2004; Hammer et al. 2001; Wells et al. 2001; Zerjal et al. 2002). Two explanations have been put forward to account for this diversity: 1) Central Asian populations represent an incubation phase of Eurasian genetic variation prior to a split toward east and west or 2) the high diversity present in Central Asia is the result of admixture between differentiated East and West Eurasian populations (Comas et al. 1998; Chaix et al. 2008). Much of the research investigating this question has utilized Y-chromosome and/or mitochondrial DNA (e.g., Wells et al.

2001; Quintana-Murci et al. 2004). Analyses based on Y-chromosome data generally support the idea that Central Asian populations are one of the oldest on the continent (Wells et al. 2001), but were also recipients of migrations (Zerjal et al. 2002). MtDNA studies, on the other hand, suggest that Central Asia has received diversity from neighboring areas, resulting in high levels of genetic diversity (Comas et al. 1998, 2004; Quintana-Murci et al. 2004).

The current project utilizes a large sample of mtDNA control region sequences from Central Asia and the surrounding areas to get a broader understanding of the distribution of genetic variation in Central Asia. This is the first time mtDNA control regions have been used to examine the genetic variation in Central Asia. The analysis of mtDNA control regions allows for more detailed analyses of evolutionary relationships than sequencing only the HVS-I region, which is the more traditional approach in local population studies (Cui et al. 2013).

Q2: What, if any, geographic barriers have or continue to affect population interactions in Central Asia?

The amount of human genetic variation between populations; although small, is of interest in the understanding of human history (Cavalli-Sforza et al. 1994). The distribution of classical markers has been studied extensively in several parts of the world and generally shows continuous geographic distribution patterns. These patterns are typically considered the result of neutral processes (Zerjal et al. 2002). However, much of the research done on global genetic variation completely ignores Central Asia

or only uses a few populations from this vast geographic span (Cavalli-Sforza et al. 1994; Pemberton et al. 2013).

There are several geographic formations that have the potential to disrupt population movements into Central Asia. These include the Altai Mountains, Caspian Sea, Himalaya Mountains, and Ural Mountains. Recent analyses by Segurel et al. (2008) found that there was no evidence of a correlation between geographic distance and genetic variation in Central Asia, but Zerjal et al. (2002) identified an east-west clinal pattern in the genetic variation based on Y-chromosome analyses. Considering these findings along with the paucity of studies utilizing Central Asian populations in global analyses, this study examines the effects of geographic distance on the structuring of genetic variation in Central Asia.

Q3: How has population history influenced the distribution of genetic variation that is seen in modern-day Central Asian populations?

An understanding of the cultural and historical background of Central Asia is necessary to make any predictions about the effects of population history on genetic variation. There are several questions that can be asked based on the history of this region. First, based on historical records, it has been conjectured that a replacement of Indo-European-speaking (Tajiks) groups by Turkic-speaking populations (Kazakhs, Kyrgyz, Turkmen, and Uzbeks) occurred throughout Central Asia. If this were true, levels of genetic similarity between Turkic-speaking populations should be higher than between these populations and Indo-European-speaking populations. The present study

addresses this question by looking more closely at the genetic relationship between Central Asian populations.

Second, Kazakhs and Uzbeks separated as distinct ethnic groups relatively recently (around the mid-1400s); as such, there should be a high degree of genetic similarity between these populations. This study examines the genetic distances between Central Asian populations to see which groups are the most similar. Last, Kazakhstan was the first area to come under the control of the Russian Empire (Dunn and Dunn 1967; Gleason 1997; Levi 2007) and has been described as the most "Russified" of the Central Asian states. The process of "Russification" is a cultural process that included the adoption of the Russian language and cultural traditions. The current research asks the question of whether this cultural transition can be evidenced in the mtDNA. In order to do this, the genetic data was examined for evidence of similarities between Kazakh and Russian mtDNA.

This project provides a better understanding of the population history and movements in Central Asia, an understudied area of the world. It utilizes a large sample of mtDNA control regions, which provides a more complete picture of the genetic variation in Central Asia than has been achieved thus far. In addition, this research provides a frame of reference for the population structure of Central Asia; one that can be used to examine Late Pleistocene population structure in future research. This is of the utmost importance and has the potential to add significantly to the recent debate on the relationship of the hominin population from Denisova, a cave site in Siberia, to other hominins as well as *Homo sapiens*. Finally, the examination of whether geographic

barriers are detected in the distribution of genetic variation in Central Asian populations can be used to test the notion that Neandertals were limited to Europe and the Middle East.

CHAPTER II

HISTORY OF CENTRAL ASIA

In this chapter, I will define Central Asia and discuss the prehistory and history of this region. Because Central Asia is such a broad term an explanation of how this region is defined in the current study is essential. In order to understand the patterning of genetic variation in Central Asia, it is necessary to discuss events in this region that have shaped population interactions. This includes a discussion of both the prehistory and history of this region. I will briefly discuss the evidence of hominin occupation in Central Asia and explain why this is important to interpretations of genetic variation in this region in the present day. For my historical review, I will focus on events that have resulted in movements of people within and through Central Asia. This includes the first documented inhabitants of Central Asia; utilization of the Silk Road as an important trade route; movement of various Turkic and Mongol groups into the area; the reign of Genghis Khan; the takeover of Central Asia by Russia, and their eventual inclusion in the Soviet Union; and lastly the reemergence of autonomous states. Accurate interpretation of the effects of population history on human genetic variation requires knowledge of the cultural, evolutionary, and historical background of this region.

What is Central Asia?

Central Asia, and other broad geographic definitions like the *Far East* and the *Middle East*, resist precise definition (Akiner 1997; Cummings 2012). Central Asia has

been defined in different ways culturally, geographically, historically, and politically (Bregel 1996; Cummings 2012; Levi 2007; Miroshnikov 1992). In its modern context, Central Asia has acquired a more specific political construction and is used as a combined term for the ex-Soviet Republics of Kazakhstan, Kyrgyzstan, Tajikistan, Turkmenistan, and Uzbekistan (Akiner 1997; Cummings 2012; Levi 2007). Because of this ambiguity it is necessary to explore exactly what is meant by the term Central Asia.

As a geographic concept, Central Asia has a long history (von Humboldt 1843). Writing in 1843, the famous geographer Alexander von Humboldt framed the classic geographic definition of Central Asia. He described Central Asia as a distinct region based on its interior drainage system and the surrounding mountain chains. Von Humboldt (1843) defined Central Asia as the area between the Caspian Sea and the Greater Khingan Range, from east to west, and from the Altai Mountains in the north to the Himalayas in the south. Von Richtofen (1877) and Mushketov (1886) excluded the western-most parts including the Aral and Caspian basins from this definition. Later, Obruchev (1951) removed the Tibetan Plateau and the Kunlun Mountains because he considered Central Asia to be delineated as an area without a water outlet to the sea. Murzaev (1958) included modern-day Kyrgyzstan, Tajikistan, Turkmenistan, and Uzbekistan, as well as the adjacent parts of Kazakhstan and the area south of the Aral Sea and Lake Balkhash. Suslov (1947, 1954), on the other hand, included the four republics and the southern and central portions of Kazakhstan only.

There is a close relationship between the cultural and the geographic delineation of Central Asia (Krader 1971). Culturally, the traditional people of Central Asia were the

Karakalpaks, Kazakhs, Kyrgyz, Tajiks, Turkmen, and Uzbek, as well as a number of other smaller groups living among them. The main difference between the cultural and geographic definitions lies in the fact that Kazakhs live in the steppe zone, which today makes up the northern part of Kazakhstan and has not always been considered a part of Central Asia, at least by Soviet scholars (Murzaev 1958; Wheeler 1964). This steppe zone merges into the forest-steppe of southern Siberia, but forms a part of the background of the cultural history of Central Asia (Krader 1971).

Politically, the term Soviet Central Asia, also Russian or Western Turkestan, has been used and refers to the areas made up of Kyrgyzstan, Tajikistan, Turkmenistan, and Uzbekistan. This terminology has been used by both Tsarist and Soviet geographers (Krader 1971; Wheeler 1964). The steppe region, today known as the republic of Kazakhstan, has historically been treated as a separate area according to Soviet political classification (Krader 1971; Wheeler 1964).

For the purposes of this project, I will define Central Asia as being made up of the republics of Kazakhstan, Kyrgyzstan, Tajikistan, Turkmenistan, and Uzbekistan (Figure 1). This is a geopolitically based definition of Central Asia and is based on contemporary political boundaries. Additionally, it has been chosen to coincide with much of the research done in this region today (Abazov 2008; Akiner 1998; Comas et al. 1998; Comas et al. 2004; Cummings 2012; Segurel et al. 2013). Geographically, this includes the areas of Kazakhstan, Kyrgyzstan, Tajikistan, Turkmenistan, and Uzbekistan, and is bounded to the west by the Caspian Sea, Afghanistan and Iran to the south, China to the east, and to the north by Russia. Ethnically, this definition includes

Kazakhs, Kyrgyz, Tajiks, Turkmen, and Uzbeks. There are other ethnic groups that have traditionally occupied Central Asia including the Karakalpaks, but for the purposes of this study I will be including only the most populous indigenous ethnic groups from this region.

FIGURE 1. *Map of Central Asia*

(Map data created by ©2018 Google)

Prehistory of Central Asia

There is archaeological evidence that Central Asia has been occupied since at least the Lower Paleolithic (Glantz 2010; Ranov et al. 1995; Ranov and Davis 1979; Zerjal et al. 2002). Remains of Lower Paleolithic cultures have been found throughout Central Asia including the Kul'dara, Karatau, and Lakhuti localities in Tajikistan (Alpysbaev 1979; Glantz 2010; Ranov and Schafer 2000; Ranov et al. 1995) and the Koshkurgan site in Kazakhstan (Derevianko 2006; Derevianko 2003; Glantz 2010), all of which have been radiometrically dated. Additionally, there is plenty of evidence of occupation during the Middle Paleolithic, including at Teshik-Tash, a location in Uzbekistan at which Neandertal remains have been uncovered (Glantz 2010; Okladnikov 1939). The Upper Paleolithic in this region, however, is not well represented and sites like Samarkandskaya, an open air Paleolithic site within the city limits of Samarkand in eastern Uzbekistan, that can be identified as Upper Paleolithic based on tool technology actually date closer to the Mesolithic boundary (Ginzburg and Gokhman 1974; Glantz 2010). There are a variety of explanations as to why this might be the case including the suggestion by Ranov and Davis (1979) and Davis and Ranov (1999) that the local environment became too harsh to support human occupation. Another explanation is that local Upper Paleolithic traditions in the region preserved a Middle Paleolithic tool kit, but are not identifiable as such because there is no radiometric information available (Glantz et al. 2006; Glantz 2010).

There are many lingering questions regarding hominin occupation in Central Asia including dates of occupation, groups of hominins present, timing and routes of

dispersal of modern humans, and the distribution of Neandertals, to name a few (Bailey et al. 2008; Glantz et al. 2009; Glantz 2010). Dates of 1.6 million years from the Nihewan basin in northern China (Zhu et al. 2004) make it surprising that the dates in Central Asia are so much younger (Kul'dara dates to 800-900 thousand years), especially since this region is a possible corridor to the east (Glantz 2010). The questions of the Neandertal status of Teshik-Tash as well as the taxonomic affinity of the hominin population at Denisova, a cave in the Altai Mountains of Siberia, Russia further raise questions about the types of hominins present in Central Asia (Glantz et al. 2009; Matthias et al. 2012; Reich et al. 2010). Despite evidence of a lengthy period of occupation, the role that Central Asia played in *Homo sapiens* origins and settlement and the route and timing of early *H. sapiens* dispersals in this region is much less clear (Comas et al. 2004; Derevianko and Markin 1992).

In contrast to the paucity of research on the peopling of Central Asia, quite a bit of research has been conducted on the peopling of Eastern Eurasia (Hanihara and Ishida 2009; Omoto 1995; Su et al. 1999) and Western Eurasia (Arredi et al. 2007; Simoni et al. 2000; Sokal et al. 1989; Tambets et al. 2000). Both genetic and morphological studies have shown that East Asia was most likely peopled in a south to north direction in which early *H. sapiens* were present in Southeast Asia by around ~60,000 years ago and from which there was an expansion northward to other parts of eastern Asia and subsequently Siberia (Su et al. 1999). In the case of the peopling of Western Eurasia, studies have shown that Europe was mostly likely peopled in a south to north and east to west direction. There were likely two waves of migration; one, during the Upper Paleolithic

and a second during the Neolithic (Arredi et al. 2007; Sokal et al. 1989; Torroni et al. 1996).

Given this information, the lack of information regarding Central Asia's role is an even more important question to answer. It is impossible to fully understand the route, timing, and patterns of early human dispersals without knowledge of how Central Asia was peopled. Additionally, with the recent boom in ancient DNA studies (Ho 2016; Prüfer et al. 2017; Skoglund et al. 2017) and the findings that Neandertal DNA (Sankararaman et al. 2012) and DNA from the hominin population at Denisova (Matthias et al. 2012) are present in contemporary human populations, it becomes more important to understand the peopling of Central Asia so that we can better interpret the interactions between these different groups of hominins.

Because of its centralized location on the Eurasian landmass, Central Asia has played a key role in the spread of early humans as well as the more recent settlements of populations across Eurasia (Martinez-Cruz et al. 2010). An examination of the genetic variation in Central Asia can help to answer questions as to the route and patterns of peopling in this region (Martinez-Cruz et al. 2010; Quintana-Murci et al. 2004). In addition, it can help to answer questions about the relationships between different groups of hominins (i.e., *Homo erectus*, Neandertals, the population represented by the Denisova Cave specimens, and *Homo sapiens*) who were all present in Eurasia during the Late Pleistocene and likely interacting with one another in areas like Central Asia where their home ranges would have overlapped.

Historical Background of Central Asia

As the present study analyzes genetic variation in Central Asia and attempts to answer the question of how that variation is patterned, it is necessary to include information on the important historical events that have shaped population interactions in this region. I will focus primarily on a discussion of events that have influenced the formation of ethnic identities as well as events that have resulted in movements of people within and through Central Asia. I will begin my discussion with the first historically cited occupants of this region.

Earliest Inhabitants of Central Asia

The Scythians, Indo-European-speaking peoples possessing European morphological features, have been cited by classical Greek and Chinese historic texts as the first inhabitants of Central Asia (Beckwith 2009; Gleason 1997; Grousset 1970; Jettmar 1998). Scythians were nomads that occupied the central Eurasian steppes from about the 9th century BCE until the 4th century CE (Rolle 2011; Sinor 1990; West 2009). They were geographically divided into distinct groups; however, they were joined by common cultural expressions (Damgaard et al. 2018). Their territory ranged from the northern Black Sea to the North Caucasus and into Central Asia. The classical Scythians occupied the northern most areas, while other Scythian groups, referred to by the Persian term Saka, lived in Central Asia (Drews 2004).

The origins of the Scythians are much debated, but Damgaard et al. (2018) summarize three main models. First, they came from the northern Caucasus or steppe

region (Grakov et al. 1977; Kristiansen 1998). Second, they originated in southern Siberia or east-central Asia (Alekseev 2006). Lastly, Scythians are a product of multiple local transitions (Bashilov and Yablonsky 2000; Unterländer et al. 2017). Damgaard et al. (2018) found that the genetic variation of Scythian groups from the Iron Age was highly structured, with diverse origins from European farmers, Late Bronze Age herders, and southern Siberian foragers. The authors also discovered a clear separation between Hungarian (western) Scythians and the Sakas (Damgaard et al. 2018).

Scythians eventually came to control the entire steppe zone, extending from the Carpathian Mountains in the west to central China and south Siberia in the east, effectively creating the first Central Asian nomadic empire (Beckwith 2009; Rolle 2011). They played an important role in the development of the Silk Road, a vast trade network connecting East to West that was in use, on and off, until the mid-1400s (Beckwith 2009; Elisseeff 2000). Although successful for a time, the western Scythians were gradually conquered by the Sarmatians after the 4th century BCE and many of the Saka migrated to South Asia after attacks by the Yuezhi, Wusun, and Xiongnu in the 2nd century BCE (Beckwith 2009). In Eastern Europe, the Scythians and the closely related Sarmatians were ultimately assimilated with the Proto-Slavic population of the region (Brzezinski and Mielczarek 2002; Mallory and Adams 1997). The Saka largely disappeared from Central Asia around two thousand years ago, but this was most likely a cultural transition that corresponded with the migration of the Xiongnu, a confederation of nomadic peoples that occupied the eastern steppes beginning in the 3rd century BCE (Damgaard et al. 2018).

Recent genetic analysis of ancient as well as modern DNA has characterized the genomic history of the Eurasian steppes as one of gradual transition. Over millennia, there has been a change in the genetic composition in this region from Bronze Age pastoralists with West Eurasian ancestry to nomadic warriors of increased East Asian ancestry (Damgaard et al. 2018). This applies to the current study because it asks questions of population structure and population history in Central Asia. I have only used contemporary mtDNA sequences and, as such, it is beyond the scope of this study to identify potential genetic links with this region's earliest inhabitants. However, I am able to examine the genetic variation within modern Central Asian populations and identify genetic links with populations from East Asia (Mongolia) and Europe (Hungary) that would provide evidence of a connection with the Scythians.

Today, Tajiks appear to be the longest standing residents of Central Asia (Beckwith 2009; Subtelny 1994; Wheeler 1964). Although they may not be the earliest inhabitants of this region, the ancestors of the Tajiks have lived there for longer than any other nationality (Bergne 2007; Bowles 1977; Levi 2007). Archaeological evidence suggests that around 2000 BCE groups of Indo-Iranian tribes slowly moved southward from what is today Russia (Akiner 1997; Grousset 1970; Levi 2007). These tribes gradually emerged as the dominant ethnicity across sedentary Central Asia as well as the steppe. Those peoples who preceded them were either displaced or absorbed into Indo-Iranian tribal societies (Canfield 1991; Hiro 2009; Levi 2007). Iranian peoples held a mostly uncontested position in these areas for about 2,500 years, giving rise to vast nomadic confederations in the steppes and sedentary empires to the south—these are the

ancestors of the modern Tajiks (Bergne 2007; Levi 2007). Among Central Asian populations in the current study, Tajiks have occupied this area for the longest period of time and, as such, I expect to find evidence of high levels of genetic diversity, which would support the hypothesis that they are an old population.

Ancient Era (2000 BCE to 155 CE)

In the 2nd and 1st millennia BCE, a succession of powerful states grew on the periphery of Central Asia launching several attacks against the nomadic steppe tribes, but rarely meeting with much success. The Median Empire, an empire formed in northwestern Iran that rose to power between 800 and 700 BCE, and the Achaemenid Empire, an empire based in Western Asia from 550 to 330 BCE, both ruled parts of Central Asia, bringing Iranian peoples into contact with the peoples of Central Asia (Daryaee 2012). Other empires, like the Macedonian and Persian empires, made inroads into Central Asia, founding cities and acquiring control of trade centers (Beckwith 2009; Sahadeo 2003).

By the 6th century BCE, there were two great kingdoms in Central Asia. Cyrus the Great, a Persian monarch, had established the city of Cyropolis along the banks of the Syr Darya River and the Bactrian Kingdom, centered in modern-day Afghanistan, was exerting influence north into the valleys of the Amu Darya River (Beckwith 2009; Gleason 1997; Grousset 1970). Prior to the 5th century, the nomadic steppe peoples were predominantly Iranian, but as Iranian civilization thrived in sedentary Central Asia, a new group of nomadic peoples emerged (Grousset 1970). A confederation of Turkic

tribes from the area around the eastern Altai Mountains arose in the middle of the 5th century and moved westward. This Turkic confederation began to exert pressure on the numerous nomadic groups on the Iranian steppes (Beckwith 2009; Grousset 1970; Levi 2007).

In the middle part of the 4th century BCE, Alexander the Great made his way through Central Asia on his quest to conquer India. The Central Asia that he passed through was already made up of multiple city-states (Gleason 1997). He founded Alexandria Eschate in 329 BCE in modern Tajikistan, spreading Hellenistic civilization deep into Central Asia (Prevas 2004). Although Alexander's stay was relatively short, Greek influence in the area lingered long after his departure (Gleason 1997). The Seleucid Empire, a Hellenistic state that existed from 312 BCE to 63 BCE, assumed control of part of Central Asia after the death of Alexander in 323 BCE (Sherwin-White and Kuhrt 1993). In 250 BCE, the Central Asian piece (Afghanistan, Tajikistan, and Uzbekistan) of the empire seceded as the Greco-Bactrian Kingdom and had widespread contact with both China and India until 125 BCE (Baumer 2012).

As Greek power subsided after the death of Alexander, Central Asia fell for a time under the influence of the Parthian empire (247 BCE to 224 CE), an important Iranian cultural and political power in ancient Iran and Iraq that, at its peak, stretched from the northern Euphrates to eastern Iran (Schulde and Reubin 2017). The Kushan Empire formed by the Yuezhi (a nomadic people of possibly Indo-European, Iranian, or Tocharian origin who migrated from Gansu and settled in ancient Bactria) flourished

across a wide band of the region from the 2nd century BCE to the 4th century CE (Mallory 1989; Mallory and Adams 1997).

Following the succession of numerous empires with interests in Central Asia, the Xiongnu Empire can be regarded as a Central Asian empire (Baumer 2014). The Xiongnu were a confederation of nomadic tribes inhabiting the eastern Eurasian steppe, centered around modern-day Mongolia, from the 3rd century BCE to the late 1st century CE (Beckwith 2009; Grousset 1970). The origin of the Xiongnu and their connection with later groups in Central Asia is not clear; however, based on archaeological evidence, a system of exchange existed between the Xiongnu elite and populations all the way from Afghanistan to China (Honeychurch and Amartuvshin 2006). Morphologically, skeletons from burial sites in Mongolia that have been attributed to the Xiongnu share similarities with Mongolians, Xianbei (China), Yakut (Siberia), and Kazakhs (Schmidt and Seguchi 2016). In addition, ancient DNA analyses have revealed a close biological similarity between the ancient Xiongnu and modern Mongolians (Keyser-Tracqui et al. 2003; Keyser-Tracqui et al. 2006). A common Y-chromosome haplogroup in Europe and an mtDNA haplogroup with high frequency in Central Asia have also been identified in the ancient Xiongnu (Kim et al. 2010). Taken together, this provides evidence of gene flow among the Xiongnu and west Eurasian groups including peoples from Central Asia and West Eurasia.

To summarize the ancient era in Central Asia, starting in 2000 BCE groups of Indo-Iranian tribes slowly moved southward from what is today Russia and expanded into Central Asia, becoming the dominant ethnicity across Central Asia (Akiner 1997;

Grousset 1970; Levi 2007). These tribes were subjected to numerous conquests by foreign (Macedonian, Persian, and Seleucid Empires) as well as localized powers (Xiongnu). This is of importance to the current study because as I examine patterns of genetic variation and assess the genetic relationships between Central Asian populations and their neighbors I will be looking for evidence of ties with some of these groups, specifically Chinese, Iranians, Mongolians, and Siberians. I have not included a Greek sample in my study, but I will look for a small genetic distance between Central Asians and Albanians and Romanians - the two populations included in this study that have the closest genetic ties with Greeks (Lao et al. 2008; Novembre et al. 2008).

Chinese, Islamic, and Turkic Influences in Central Asia (4^{th} – 9^{th} centuries)

After the end of the Xiongnu and Kushan empires, there began a new stage of history in Central Asia characterized by the movement of nomadic groups from the north and east into and through Central Asia. In the 4^{th} century, the Huns, a group of Turkic-speaking nomads, began to move from Mongolia westwards (Frye 1996). During the 5^{th} century, there were increased movements of a number of Hun tribes, from the northern steppes into Bactria, which was defined as an area north of the Hindu Kush mountain range and south of the Amu Darya River encompassing the flat region of modern Afghanistan, Tajikistan, and Uzbekistan (Grousset 1970). Iranian-speaking tribes were included in the movement and by the next century Turkic-speaking groups had largely replaced Iranian tribes on the steppes (Frye 1996).

Beginning in the mid-5th century, another wave of Turkic-speaking tribes – the Hephthalites, originally from the Altai-Mongolia area, moved across Central Asia on their way to invade India. The Turks, whose center was in the Altai Mountains, began to extend their influence over neighboring tribes in Mongolia and the western steppe in the middle of the 6th century (Frye 1996). Led by Ishtemi, a Turk army moved south, defeating the main Hephthalite force in the process (Frye 1996; Grousset 1970; Sinor 1990). The Sasanians (successors to the Parthian Empire) assisted the Turks and divided the Hephthalite domains. The Turks took over the lands to the north of the Oxus River, while the Sasanians ruled over the south (Frye 1975a; Frye 1996; Sinor 1990).

Thus, by the end of the 7th century, in Mongolia and the western steppes numerous tribes of nomads had moved westward, extending their rule over the Tarim Basin and Transoxiana (modern-day Tajikistan, Uzbekistan, south Kyrgyzstan, and southwest Kazakhstan). Turkish chiefs had gone as far south as the mountains of present-day Afghanistan, but Bactria was considered outside of the dominion of the Turkish state. Overall, the settled peoples under the control of Turkish rulers remained Indo-Iranian-speakers (Frye 1996; Grousset 1970).

During this same time frame, the Sui and later the Tang dynasties in China began to make attempts to expand into Central Asia. Chinese foreign policy had to contend with Turkic nomads, who were becoming the dominant ethnic group in the region (Ebrey and Walthall 2006; Ebrey 2010). In an attempt to avoid threats from the Turks, the Sui overhauled fortifications, accepted trade and tribute missions from the Turks, and sent royal princesses to marry Turkic clan leaders (Benn 2002). The Turks were a major

militarized force and were employed by the Chinese as early as the Sui Dynasty (581-681 CE). In 605 CE, a Chinese general led 20,000 Turks against the Khitan (a nomadic people from Northeast Asia), who had begun raiding northeast China. The Turks received livestock and Khitan women as a reward for their aid (Ebrey 2010).

After a number of internal conflicts in China were successfully resolved in 628 CE, the Tang began an offensive against the Turks, capturing part of the Ordos Desert, southern Mongolia, and present-day Inner Mongolia (Ebrey 2010). After this victory, the Turks in the region promised allegiance to the Chinese empire (Benn 2002). The Chinese government adopted the policy of dominating the central steppes, and, with the help of allies like the Turkic Uyghurs, the Tang Dynasty conquered Central Asia in the 640s and 650s (Ebrey and Walthall 2006). The expansion into Central Asia continued under successive emperors and lasted until 670 CE, when the Tibetan Empire began to compete for control of Central Asia (Millward 2007).

In the 8th century, Islam began to diffuse into Central Asia. The desert nomads were able to militarily compete with the steppe nomads, and the Arab Empire obtained power over areas of Central Asia. Early conquests were overturned by indigenous uprisings and attack by the Turgesh, a Turkic tribal confederation. The collapse of the Turgesh Khaganate beginning in 738 CE paved the way for Muslim authority to be imposed once again (Bregel 2003; Golden 1992). The Arab invasion resulted in the Chinese influence being removed from western Central Asia, and Islamic influences would dominate the region for the next several centuries. However, large-scale Islamization did not start until

the 9th century, with the emergence of local Iranian and Turkic dynasties like the Samanids (Bartol′d 1977; Frye 1975b).

The Samanid Empire was a Sunni Iranian empire that ruled from 819 to 999 CE (Frye 1975a). The empire was predominantly centered in Korasan (an area in the northeastern part of Greater Persia including part of Central Asia and Afghanistan) and Transoxiana (modern-day Tajikistan, Uzbekistan, southwest Kazakhstan, and southern Kyrgyzstan), but at its greatest extent, it encompassed all of present-day Afghanistan, and large parts of Iran, Kazakhstan, Kyrgyzstan, Pakistan, Tajikistan, Turkmenistan, and Uzbekistan (Frye 1996; Taagepera 1997).

The Samanids revived Persian culture and brought Iranian traditions into the Islamic world (Canfield 1991). They also spread Sunni Islam, dispersing Islamic architecture and Islamic-Persian culture into the heart of Central Asia (Canfield 1991; Frye 1975a; Frye 1996). Although Islam had been introduced to Central Asia earlier during the Islamic conquest of the region in the early 8th century (Brower 1997; Suleimanov 2007), the influence of the Samanid Empire played a large role in the widespread adoption of Islam. In fact, during the 9th century, after the first complete Persian translation of the Qur'an, populations under control of the Samanid dynasty began accepting Islam in significant numbers (Dillon 2004). The introduction of Islam into Central Asia had a profound impact on the indigenous cultures in the region, making them a part of Islamic civilization (Jackson 2017).

Taken as a whole, between the 4th and 9th centuries, Central Asia was influenced by numerous population movements into and through the region. Beginning with Turkic

tribes like the Hun and Hephthalite, Turks began to become the dominant ethnic group in the region, but settled groups primarily remained Indo-Iranian-speakers. The Turks fought with the Sui and Tang Dynasties and later the Arab Empire to maintain control in Central Asia. This period in history is characterized by a wide array of population interactions within Central Asia. These historical events are likely to be captured in present-day population variation in the following patterns: 1) Turkic-speaking groups (Kazakhs, Kyrgyz, Tajiks, and Uzbeks) should have a smaller genetic distance with the Chinese than Tajiks because their ancestors (i.e., the Turks) were the primary group interacting with the Sui and Tang dynasties and 2) Central Asian populations should show evidence of gene flow with Arab populations from the Arabian Peninsula, and because all Central Asian populations adopted Islam as the primary religion there should not be any significant difference in the genetic distances among the Central Asian populations and groups from the Near East.

Formation of Ethnic Identities

In the year 999, a confederation of pastoral nomadic Turkic Muslims called the Qarakhanids entered Bukhara, a city in Uzbekistan (Hiro 2009; Levi 2007). This marks the early stages of Turkicization, "the long process by which Turkic language speakers gradually became the dominant population of the region as they either subsumed the Iranian-speaking Tajiks or relegated them to the mountainous periphery of the Upper Oxus Valley, the territory that is today Tajikistan" (Levi 2007: 19), of sedentary Central Asia (Akiner 1997; Bregel 1996; Levi 2007).

By the end of the 11th century, the Oghuz, another group of Turkic pastoralists, emerged as the dominant population across much of Central Asia and the Middle East (Grousset 1970). The designation of Turkmen began to be applied to Muslim Oghuz Turks during this period. Today, the Turkic populations of Turkey and Azerbaijan are of similar ancestry to the Turkmen in Central Asia, but the designation "Turkmen" only applies to the descendants of the Central Asian Oghuz tribes (Levi 2007).

In the mid-6th century, further to the east, the Kyrgyz confederation of Turko-Mongol tribes was the dominant power in the Upper Yenisei River region of Siberia. They maintained that power through much of the 9th and 10th centuries (Beckwith 2009; Bregel 1991; Levi 2007). Late in the 12th century, a young Mongol warrior named Temujin, better known as Genghis Khan, slowly rose in power and compelled many of the Turkic and Mongol tribes of the region, including the Kyrgyz to accept his authority (Weatherford 2004). The rise of Genghis Khan and his conquest of Central Asia resettled countless Turks and Mongols from the northern steppe to the south (Bowles 1977; Levi 2007). Migratory groups like the Kyrgyz were active participants in the Mongol conquests and eventually abandoned their Siberian homeland for the Tien Shan Mountains, settling in the area that is modern Kyrgyzstan (Levi 2007).

Following Genghis Khan's death in 1227, the Mongol Empire was divided among the royal family into four ulus. Genghis Khan's eldest son, Jochi, died before him and so his heirs were granted control over the northern steppe as far to the west as the Mongol troops could conquer (Weatherford 2004). This would become the Qipchaq Khanate and is the homeland of the Uzbeks and Kazakhs (Levi 2007). Later, a portion of

the Qipchaq Turkic tribes converted to Islam under the leadership of Uzbek Khan and it is likely that the ethnic designation of 'Uzbek' is derived from his name (Cecen 1999; Levi 2007). Even after the death of Genghis Khan, much of his empire continued to be dominated by his successors. But, in 1369, Turkic leader Timur (Tamerlane) conquered much of the region (Marozzi 2005). During Timur's reign, the Central Asian nomadic steppe culture merged with the settled culture of Iran. Soon after Timur's death, his large empire collapsed and the region became divided into smaller Khanates, including the Khanate of Bukhara, Khanate of Kashgar, Khanate of Khiva, and Khanate of Kokand (Grousset 1970; Manz 1998; Marozzi 2005). In 1456, a new power arrived from the east and attacked the Uzbeks. The Uzbek leader survived this humiliating defeat, but his position of authority was irreparably damaged and a portion of Uzbek tribes defected; the defectors became known as Kazakh-Uzbeks or just Kazakhs (free men) (Levi 2007).

It has been argued that between the 14th and 16th centuries, the merging of disparate tribes of Central Asia into nations occurred (Akiner 1995; Akiner 1997). This was a complicated process and there are issues of historiography; however, by the end of this period, some groups appear to have acquired a degree of internal cohesion that makes it possible to speak of 'the Kazakhs' or 'the Turkmen' (Akiner 1997). It is important to keep in mind that this well-ordered picture is mostly a modern construct; it gives the impression of continuity, historical inevitability, and order, and ignores awkward ambiguities, the changeable nature of tribal formations, and the continuing process of assimilation and fragmentation (Akiner 1997). Prior to this time frame, people's identities were more focused on regional and tribal based identities rather than a

broader ethnic identity (Schatz 2000; Tishkov 1997). Ethnic identities were likely distinctly defined at the micro-level, but at the macro-level there was a certain amount of fluidity and an absence of recognized demarcation (Akiner 1997).

The formation of ethnic identities in Central Asia was a complicated process and one that is marked by ambiguity and fluidity. As such, populations in Central Asia should be genetically very similar. Despite this similarity, it is possible to make some predictions regarding the effects of population history on the genetic variation in this region. First, because Tajiks have a different origin than the Turkic-speaking groups, they should be genetically distinct (have a larger genetic distance) from other Central Asian populations. Turkic-speaking groups expanded into Central Asia and gradually became the dominant ethnic group in the region. As a result, Tajiks were assimilated, displaced, or replaced. An examination of the levels of genetic diversity in the Tajiks will be able to answer questions as to how the movement of Turkic-speaking groups into Central Asia affected Indo-European-speaking peoples (Tajiks). Second, until relatively recently (1456) Kazakhs and Uzbeks were not differentiated tribes. Therefore, the genetic distance between these two populations should be small reflecting their shared ancestry. Third, the Turkmen share ancestry with Turkic populations in Azerbaijan and Turkey. Accordingly, the genetic distance between Turkmen and Turks and Azerbaijani should reflect this genetic similarity. Lastly, because the Kyrgyz were originally from the Siberian region and settled in modern-day Kyrgyzstan only after the conquests of Genghis Khan, this population should demonstrate small genetic distances with groups from Siberia.

Russian Conquest of Central Asia

In the 14th and 15th centuries, important changes to the world economy began to occur as the result of the development of nautical technology and the introduction of gunpowder. Europeans pioneered ocean trade routes, and long distance trade connecting Western Europe to India and East Asia began to travel increasingly over water and not overland through Central Asia (Beckwith 2009; Elisseeff 2000). However, the rise of Russia as a world power allowed Central Asia to maintain its role as a channel for trade, connecting Russia with India (Baumer 2014; Levi 1999). The introduction of gunpowder permitted settled populations to defeat the steppe nomads for the first time and, as a result, beginning in the 15th century, the domain of the nomads began to shrink as settled powers gradually began to conquer Central Asia (Andrade 2016).

Russia's rise as an expansionist empire began in 1480, but it took some time before Central Asia came under Russian control (Dunn and Dunn 1967; Gleason 1997). From 1582-1639, Cossacks (a group of East Slavic-speaking people mainly located in southern Russia and southeastern Ukraine) traveled into Siberian forests, marking Russia's first real contact with Central Asia. At this time, Russia did not expand south for two main reasons: 1) the Siberian Cossacks were unfamiliar with the steppe terrain and 2) the steppe nomads were numerous and warlike in contrast to the greatly outnumbered indigenous groups in Siberia (Forsyth 1992). In 1730, the first Russian advance into Central Asia occurred with the acceptance of Russian power by Abu'l-Khayr, khan of the Lesser Horde. This did not provide the Russian government with much real control of the Kazakh steppe; however, it carried with it the expectation of

domination and served as a justification for additional advance to defend Russian settlers and to punish Kazakh uprisings (Manz 1994).

The gradual process of the conquest of the remainder of Central Asia by the Russian Empire began in the early 19th century. The steppe peoples were largely unable to contest the Russian advance; although, the Kazakhs of the Great Horde mounted a rebellion from 1837 to 1846 (Hambly 1969). Despite this, by the end of 1846, the Russian Empire included virtually all of the territory of modern Kazakhstan (Dunn and Dunn 1967; Gleason 1997; Levi 2007).

The second wave of Russian expansion in Central Asia began in 1865 with the subjugation of Tashkent, located in northeast Uzbekistan, and the subsequent securing of the frontier. The Russians slowly appropriated large sections of the steppe and gave them to Russian farmers, who began arriving in large numbers (Hambly 1969), and, by 1884 the conquest of Central Asia was effectively completed (Levi 2007). Although the process of moving Russian farmers into Central Asia was at first restricted to the northern outskirts of the steppe, in the 1890s large numbers of Russians settled farther south, particularly in the southeastern part of modern Kazakhstan (Hambly 1969). While the Russian regime left significant parts of the previous regimes intact and maintained a general policy of trying not to interfere in the everyday lives of their Central Asian subjects, their impact was nevertheless tremendous (Akiner 1997; Hambly 1969; Hirsch 2005; Levi 2007).

The conquest of Central Asia by the Russian Empire is likely to be captured in the patterns of genetic variation in Central Asia in the following way: because the

history of Russian conquest began first in the steppes, a more substantial impact of Russian influence on the genetic variation amongst Kazakhs is expected than in the other Central Asian populations.

Central Asia under Soviet Rule

Following the Russian conquest and soon after the success of the Bolshevik revolution and the founding of the Soviet Union, Central Asia peoples were divided into new, ethnically based political units corresponding to the provisions of the national delimitation of states (Diener 2002; Levi 2007). Initially, the Bolsheviks established the Turkestan Autonomous Soviet Socialist Republic (SSR). Beginning in 1920, efforts were made to divide the region further to limit threats like Pan-Turkism and Pan-Islamism (Wheeler 1964). In 1920, the Kirghiz Autonomous SSR, including modern Kazakhstan, was established. In 1925, it was renamed the Kazakh Autonomous SSR. In 1924, both the Uzbek SSR and the Turkmen SSR were created. In 1929, the Tajik SSR was separated from the Uzbek SSR. Finally, in 1936 the Kyrgyz Autonomous SSR was established. These borders did not have much to do with ethnic make-up, but instead were created to introduce division and conflict amongst Central Asian peoples (George 2009; Khalid 2006; Wheeler 1964). Under the Soviets, the local cultures and languages were categorized and codified and their distinctions not only delineated, but encouraged (Cummings 2012; Wheeler 1964).

After the creation of titular republics by the Soviet Union, the process of creating modern Soviet Central Asian identities was undertaken in the form of creating

nationality, or in Soviet usage, ethnic identity (Akiner 1997). Soviet language emphasized nationality in place of what is generally thought of in anthropological terms as ethnic identity. In other words, Soviet authorities conflated ethnic and national identities with the term nationality (Rasuly-Paleczek 1998). As a part of this process, national languages were created to foster group integration, national histories were compiled that outlined the development of ethnic groups from prehistory to the present, and a concerted effort was made to eradicate the cultural heritage of the past, namely Islam (Akiner 1997). Implicit in the entire process was the understanding that ethnic groups were based on perceived biological differences or a shared ancestry.

During the Soviet period, there were many important movements of populations that are relevant to the current study. This includes, of course, the continued movement of Russians into Central Asia. During WWII, several million Soviet citizens and hundreds of factories were evacuated to the comparative safety of Central Asia. This evacuation concentrated on shifting essential wartime industry and the factory workers in charge of such production. Entire factories along with their employees were transported by railway to cities like Tashkent in Uzbekistan (Manley 2009). As a result of the war with Germany, Soviet officials implemented a deportation policy along ethnic lines. Initially, Soviet citizens of German descent were deported to Central Asia, including a large portion that was sent to Kazakhstan. As many as 220,000 German deportees were enlisted in a "labor army" that performed a number of duties including working at construction sites developing infrastructure (Polian 2004). In the latter part of WWII, a new wave of deportation commenced and included Karachays, Kalmyks,

Chechens, Ingush, Kabardians, and Crimean Tatars, who were deported to Kazakhstan, Kyrgyzstan, and Uzbekistan (Polian 2004). Starting in 1954, the Virgin Lands Campaign, a large-scale Soviet agricultural resettlement program, moved more than 300,000 people, mostly from the Ukraine, to the territory of Central Asia, primarily to the northern Kazakh SSR (Dave 2007b). All of these events changed the ethnic makeup of the populations in Central Asia, especially in Kazakhstan. By 1959, around 60% of Kazakhstan's population was Russian-speaking peoples – 43% Russians and the remaining 17% were Belarusians, Germans, and Ukrainians (Dave 2007b). Also of importance, during the Soviet period there was an emphasis placed on harmony between nationalities, which led to increased acceptance of intermarriages (Abazov 2007).

During the Soviet period, Central Asia experienced a significant degree of population influx not only from Russians, but also other groups including Germans and Ukrainians. Although Central Asia has always been the location of extensive gene flow, during the Soviet period gene flow from different ethnic groups is introduced. This should be apparent in the genetic structure of Central Asian populations. In particular, Kazakhstan experienced the highest degree of immigration and, if there were significant levels of intermarriage, there should be a high level of genetic diversity present in this population, indicative of admixture. Additionally, Kazakhs should have a small genetic distance with Russians, but also with Ukrainians, Belarusians, Kalmyks, and Adygei (closely related to Kabardians and Chechens.).

Central Asian Autonomy

With the dissolution of the Soviet Union at the end of 1991, one of the main concerns of the new governments has been to form new state ideologies, which draw on the culture and traditions of the titular people (Akiner 1997). Over the past approximately 150 years, ethnic identities in Central Asia have experienced a substantial amount of reformation. They have shifted from what were "predominantly locally defined 'informal' identifications to the institutionalized 'nationalities' of the Soviet era, then to the formal nation-state identities of the 1990s" (Akiner 1997:391). Thus, ethnic identity in Central Asia might be understood as constantly shifting according to economic, political, and social conditions; and as such, it is highly situational and contextual (Rasuly-Paleczek 1998). This is something that must be remembered when examining the genetic makeup of populations/ethnic groups in Central Asia and must be factored in when interpreting the results of the current study.

Since Central Asian states gained independence in 1991, there have been significant changes to the ethnic makeup of all five countries. Currently, in all five Central Asian states, the titular ethnic groups make up the majority of the population. In Kazakhstan, emigration of Russians and Germans combined with a concerted effort to encourage immigration of ethnic Kazakhs from China, Mongolia, and Russia have resulted in Kazakhs becoming the most populous ethnic group (Dave 2007a; Sancak 2007; Sarsembayev 1999). According to the 2009 census, 63.1% of the population is Kazakh, 23.7% Russian, 2.9% Uzbek, 2.1% Ukrainian, 1.4% Uyghur, 1.3% Tatar, 1.1% German, and 4.4% other (Kazakhstan 2010; Spoorenberg 2013). Similarly in

Kyrgyzstan, the percentage of ethnic Kyrgyz has increased from 52.4% in 1990 to over 70.9% in 2009, while the percentage of ethnic groups including Germans, Russians, Tatars, and Ukrainians has decreased from 35% to roughly 7% (Republic 2009; Spoorenberg 2013). According to the CIA World Factbook (2014), 84.3% of the population of Tajikistan is made up of Tajiks, 13.8% Uzbeks, and 2% other (including Kyrgyz, Russian, Turkmen, Tatar, and Arab). In 1989, Russians made up 7.6% of the population of Tajikistan, but they are now less than 0.5%, and the German population of Tajikistan which numbered 38,853 in 1979, has almost completely vanished (Pohl 2007; Service 2010). In Turkmenistan and Uzbekistan, Turkmen and Uzbeks make up the overwhelming majority of the population in their titular states. The CIA World Factbook (2014) lists the ethnic make-up of Turkmenistan as 85% Turkmen, 5% Uzbek, 4% Russian, and 6% other (based on 2003 estimates). Lastly for Uzbekistan, The State Committee of the Republic of Uzbekistan on Statistics (2017) provides the following percentages for ethnic structure: Uzbeks 83.8%, Tajiks 4.8%, Kazakhs 2.5%, Russians 2.3%, Karakalpaks 2.2%, and less than 1% of Kyrgyz, Tatars, Turkmen, Koreans, and Ukrainians.

For the purposes of this study, it is helpful to understand the present-day ethnic composition of the states under study. This will play a role in interpreting the results of this study and identifying how population history has influenced the current genetic structure in Central Asia.

Application to this Study

Throughout history, Central Asia has been subjected to large movements of populations, some beginning from outside the region and moving inwards, others circulating outwards into neighboring areas (Akiner 1997). Both archaeological and morphological evidence indicate that there was a high level of intermarriage between groups in the region as well as a strong trend towards cultural assimilation (Akiner 1997; Gleason 1997). Currently, much of the genetic research supports this general trend as well (Calafell et al. 2000; Comas et al. 1998; Comas et al. 2004).

Based on archaeological records, Central Asia has been occupied since at least the Lower Paleolithic. The relatively more recent dates of occupation as compared to East and West Eurasia are interesting and may simply be the result of lack of data versus actual non-occupation of the region. In terms of human evolution, Central Asia's central location makes it a strategic area through which early *H. sapiens* may have dispersed. While the peopling of East and West Eurasia have been extensively researched, Central Asia's role is still poorly understood. The present research builds a foundation upon which it is possible to interpret Central Asia's possible role in the origin and dispersal of *H. sapiens* as well as answer questions about Neandertal distribution and the relationship of the hominins at Denisova to *H. sapiens*.

Although the complex history of Central Asia including migrations, warfare, and expansive interregional trade makes it difficult to make hypotheses about population history and its effect on genetic variation, there are some questions that the current study seeks to answer. First, it has been hypothesized that a complete replacement of Indo-

European-speaking (Tajik) groups by Turkic-speaking populations (Kazakhs, Kyrgyz, Turkmen and Uzbeks) may have occurred throughout Central Asia. If this is the case, the levels of genetic similarity between Turkic-speaking populations should be much higher than between these populations and Tajiks. Martinez-Cruz et al. (2010) found that this was not the case and that partial admixture appeared more likely, but the present study also addresses this question utilizing a larger, more representative sample. Second, Kazakhs and Uzbeks separated only recently (c. 1456) as distinct ethnic groups. As such, there should be a high degree of genetic similarity between these populations and they should be at least somewhat genetically distinct from other Turkic-speaking populations (Kyrgyz and Turkmen) and even more so from Tajiks. Third, because Kazakhstan was the first geographic area to come fully under the control of the Russian Empire and has been described as the most "Russified" of the Central Asian states, the genetic data should show evidence of similarities between Kazakh and Russian mtDNA. The present study addresses these questions by exploring the distribution of genetic variation throughout Central Asia. The historical events discussed in this chapter including, but not limited to, the takeover of Central Asia by foreign (Greeks, Russians) and localized powers (Xiongnu), the Islamization and Turkicization of Central Asia, and the deportation of various ethnic groups into this region during the Soviet era will all be considered when discussing the influence of population history on the genetic structure of Central Asia.

CHAPTER III

BACKGROUND ON ANTHROPOLOGICAL GENETICS AND GENETIC RESEARCH IN CENTRAL ASIA

In this chapter, I review the historical background of anthropological genetics research. Specifically, I will examine the development of anthropological genetics as a subfield of study within biological anthropology. I also review the genetic research that has been done on Central Asian populations up to this point. In so doing, I will outline the gaps that exist and how I have come to frame my project, as well as illustrate what the current project adds to the discussion.

Historical Background of Anthropological Genetics

Anthropology as an academic discipline is very young, and the use of genetics within the field has become of relevance only fairly recently (Crawford 2007; Crawford and Workman 1973; O'Rourke 2003; Spuhler 1973). The field of genetics originated just over a century ago with the rediscovery of Mendel's ground-breaking pea plant experiments (Correns 1900; de Vries 1900; Tschermak 1900), and the physical structure of DNA was revealed only a little over 60 years ago (Watson and Crick 1953). These two significant events, along with the mathematical formulation of population genetics by Fisher (1922), Haldane (1956), and Wright (1921), opened the gateway for anthropologists to begin using genetic data to study patterns of evolution and human biological variation (Crawford 2000a; O'Rourke 2003; Relethford 2003). Consequently,

anthropological genetics, the field that answers evolutionary questions using the methods and theories of genetics, can really only trace its origins back to the 1950s (Boyd 1950; Glass 1953; Hanna et al. 1953; Hulse 1955; Livingstone 1958; Mourant 1954); although, the initial joining of anthropology and genetics occurred in 1903 with Farabee's PhD dissertation in anthropology, which examined the inheritance of brachydactyly in a bilateral kinship group of 69 Pennsylvanians (Farabee 1903).

In 1901, Landsteiner discovered the ABO blood system (Landsteiner 1901). Just a couple of decades later, this discovery allowed the first examination of population variation using genetic data when Hirschfeld and Hirschfeld (1919) provided the first evidence that genetic variation was distributed geographically, which led to the recognition that population differences existed for classic genetic markers (e.g., red blood cell polymorphisms). This, in turn, meant that classic genetic markers were useful as a mechanism for studying human variation (Crawford 1973; O'Rourke 2003) and so, early anthropological genetics research utilized simple gene systems, like ABO blood groups, as a method of analysis (Brues 1963; Livingstone 1958; Livingstone 1960; Modiano et al. 1965; Mourant 1954). Some of the earliest anthropological research specifically made use of the ABO blood groups and included the pivotal work on the effects of natural selection on human polymorphisms by Alice Brues (1963) and Frank Livingstone (1958, 1960).

Prior to the late 1950s, few anthropologists were trained in human genetics. This is primarily because traditionally physical anthropologists had been trained in morphology and racial classification based on typology (Crawford 2007). Of course, this

excludes the infamous work done by anthropologists in the areas of racial serology and eugenics in the early- to mid-19th century (Davenport 1911; Haeckel 1876; Marks 2012; Mendes-Correa 1926). Despite the negative association of genetic research within anthropology with racial typology and the eugenics movement, by the late 1950s and early 1960s, many anthropologists began to have some training in human genetics and the field of anthropological genetics, distinct from the efforts of eugenicists, was in full swing (Friedlaender 1971; Giles et al. 1966; Lewontin 1967; Livingstone 1958).

In the 1960s and 1970s, there was an explosion of anthropological genetics research spurred by the inclusion of methods from human genetics into biological anthropological studies on human variation (Giles et al. 1970; Lewontin 1972; McKusick et al. 1964; Roberts 1969). It is important to recognize that the advances in the area of anthropological genetics did not come about simply as a result of borrowing genetic methods of analyses (Crawford 2007; O'Rourke 2003). Genetic methodology was enriched by the use of an anthropological perspective, which recognized the diversity of social patterns and human demography and understood the importance of carrying out long-term population studies (O'Rourke 2003).

In the mid-1960s, human genetic variation was being described chiefly through the calculation of allele frequencies for blood group loci and/or proteins (Boyd 1963; Brues 1963; Roberts 1967). Because blood typing dated back to the early 1900s, much more data were available on blood group distributions and variation than proteins (Crawford 2000a; Crawford and Workman 1973). However, in the mid-1950s, Smithies (1955) invented starch-gel electrophoresis, which allowed the more complete separation

of different sized molecules through the addition of an electric force (Smithies 1955; Smithies 1959). This led to a flurry of activity amongst anthropological geneticists as they applied this new method to a wide array of populations (Crawford 1973; Crawford 2000a; Goodman 1963; Wang et al. 1967). By the late 1960s, most anthropological genetic studies were focused on documenting local patterns of genetic variation within and between populations (Cavalli-Sforza 1969; Friedlaender 1971; Giles et al. 1966). Additionally, many studies of human population genetics were beginning to examine the effects of evolutionary mechanisms and how evolutionary forces, like genetic drift, gave rise to observed patterns of genetic variation (Cavalli-Sforza et al. 1964; Crawford 1973; Lewontin 1967; Lewontin 1972; O'Rourke 2003).

In the 1970s and 1980s, methodological and technological breakthroughs permitted the study of DNA in human populations. These breakthroughs included: 1) improvements in the methods used for DNA extraction (Rubicz et al. 2007); 2) the development of hybridization methods that made it possible to compare DNA strands (Britten and Kohne 1968); 3) the discovery that bacteria produced restriction enzymes, which permitted the subdivision of long chains of DNA into more manageable fragments (Danna and Nathans 1971; Meselson and Yuan 1968; Smith and Welcox 1970); and 4) the development of polymerase chain reaction (PCR) methodology to amplify and copy regions of DNA (Mullis and Faloona 1987; Mullis et al. 1986). These advances further revealed the existence of greater amounts of genetic variation within human DNA and radically affected the measurement and analysis of human genetic variation (Crawford 1987; Crawford 2000a; Crawford 2007). In particular, the development of PCR

methodology revolutionized the way in which data on genetic variation in populations might be obtained. Classical markers, enzymes, and proteins were replaced by direct DNA sequences, insertions and deletions, single nucleotide polymorphisms (SNPs), restriction site polymorphisms, and short tandem repeats (STRs) [(O'Rourke 2003)].

Because of these technological advances, anthropological genetics was formalized as a field of inquiry during the 1970s and 1980s, with the initial twin emphases of population structure and genetic-environmental interactions in complex traits (Cavalli-Sforza and Bodmer 1971; Crawford and Mielke 1982; Crawford and Workman 1973; Mielke and Crawford 1980). DNA markers became powerful tools for the reconstruction of human phylogeny. In particular, because of its abundance in skeletal material, lack of recombination, and maternal transmission, mtDNA proved to be a useful chronometer. This is because mtDNA is inherited essentially as a single copy that is passed only by the mother, and thus differences in mtDNA between individuals result completely from the accumulation of mutations over time (Avise 1986; Avise et al. 1979; Crawford 2000a).

The field of anthropological genetics has been swept along by the molecular revolution (Crawford 2000a) and since 1984 there has been a shift in the focus of anthropological genetics research (Crawford 2007). The unique characteristics of mitochondrial DNA and a non-recombining portion of the Y-chromosome (NRY) have made the shift in emphasis from population structure and genetic epidemiology to a study of broader evolutionary questions possible (Crawford 2003; Crawford 2007). These markers are more informative than polymorphic blood groups and proteins and

they enable the reconstruction of sex-specific migration patterns and can be used to build molecular clocks based on the accumulation of mutations over time (Crawford 2007). The development of methods to score the plethora of short tandem repeats (STRs) and single nucleotide polymorphisms (SNPs) found throughout the genome allow new questions to be posed and answers gathered (Crawford 2000a; Crawford 2007).

All of the innovations that have occurred within the past 50 or so years have made the field of anthropological genetics better and more applicable to evolutionary as well as human biological variation research because it is more reliable, easier to apply, and is less expensive. These advancements have allowed unexpected levels of variation to be revealed within and between populations. Biological anthropologists have been able to make use of genetic methods and data to ask questions concerning human variation and evolution, and to use their unique perspectives to assist in answering these questions.

Early on in the study of human genetic variation, anthropologists were able to make use of known population histories in their examinations of human genetic variation. For example, Crawford and colleagues examined the relationship between migration, population movement, and resettlement, and admixture in Tlaxcaltecan populations of Central Mexico (Crawford 1976) and among Black Carib communities in Belize and Guatemala (Crawford 1983; Crawford 1984). In addition, knowledge of historical sizes of populations was used to assess the role of genetic drift in structuring allele frequency variation in modern populations. Roberts (1967, 1968) analyzed the historical demography and changing genetic structure of the island of Tristan de Cunha,

and Cavalli-Sforza (1969) studied the effects of reduced population size and relative isolation on the genetic structure of Alpine communities in Italy. Roberts' (1967) original work on Tristan de Cunha gave valuable insight into the role of unique historical events in the molding of the gene pool of isolated human populations (Roberts 1967; Roberts 1968).

The relationship between demographic structure and dynamics have been explained by analyses that have utilized communities whose identities are related to specific religions such as the Amish (McKusick et al. 1964), Dunkers (Glass 1953), Mennonites (Crawford 2000b; Crawford et al. 1989), and Mormons (O'Brien et al. 1994; O'Brien et al. 1996). However, the study of human population genetics does not require either detailed population histories or records. Using the mathematical treatment of isolation by distance and identity by descent (Malécot 1948), Morton and colleagues were able to develop analytical methods, called "bioassay of kinship," to examine the genetic structure of many populations and regions, namely Micronesia and the Middle East (Morton et al. 1982; Morton and Lalouel 1973). Friedlaender (1971) and Neel and Weiss (1975) used similar population genetic models and methods.

The studies thus far described have all focused on local populations or groups of historically related populations, but some anthropological genetic studies were centered around examining broader patterns of variation (O'Rourke 2003). The seminal work by Cavalli-Sforza et al. (1994) pioneered studies seeking regional or continental patterns of genetic variation. Several similar studies also examined the association between patterns of genetic variation and linguistic group distribution (Cavalli-Sforza et al. 1988). In a

similar vein, Suarez and colleagues (O'Rourke et al. 1992; Suarez et al. 1985) investigated the effects of geography and ecology on variations in gene frequency in a large collection of populations from the Americas (O'Rourke 2003).

The attention to the dynamics of local populations in anthropological genetic studies was based on theory from evolutionary population genetics and anthropological interest in population history (O'Rourke 2003). Lewontin (1972) demonstrated that 85% of the observable genetic variation of 15 protein loci exists within local populations. This paved the way for an investigation of the functions of evolutionary mechanisms in the structuring of allelic variation within populations (O'Rourke 2003).

Studies in anthropological genetics have utilized molecular markers to investigate questions concerning the history of a population, population structure, and events like migration and gene flow (Rubicz et al. 2007). Human population history has been studied using both morphological (North et al. 2000; Relethford 2001) and genetic data (Cavalli-Sforza et al. 1994; Kivisild et al. 2003) and has been shown to be geographically structured at a continental level (Cavalli-Sforza et al. 1994; Rosenberg et al. 2002); although, Central Asia has largely been ignored in these analyses. Recent work has focused on mtDNA and the Y chromosome because both are haploid non-recombining loci for which in depth phylogenies can be built (Arredi et al. 2007; Calafell et al. 2000; Comas et al. 2004; Wells et al. 2001; Zerjal et al. 2002). Both have a small effective population size and reduced gene flow, which make them more vulnerable to drift than autosomal sequences (Zerjal et al. 2002). As such, as much as 30% (for mtDNA [(Jorde et al. 2000)] or 40% (for the Y chromosome [(Hammer et al.

2001; Santos et al. 1999)] of the variation in these two loci has been found between populations.

As this brief review has shown, the work of anthropological geneticists has focused on examining population structure and history, as well as examining the evolutionary history of our species. Anthropological genetics is an especially useful tool for examining questions related to genetic variation in Central Asia like: 1) What is the relationship within and among populations in Central Asia?; 2) How does the genetic variation in Central Asia fit into existing worldwide models of geographically structured variation?; and 3) How have historical events like the rule of Genghis Khan and his descendants shaped patterns of human variation? Although anthropologists have traditionally studied morphology, the paucity of skeletons in Central Asia combined with the difficulty of gaining access to the skeletal samples available make genetic data a critical means of examining the evolutionary history of populations in this region.

Current State of Genetics Research in Central Asia

From a genetic perspective, Central Asia is one of the least studied areas of the world (Comas et al. 1998; Comas et al. 2004). Morphologically, biological anthropologists have defined Central Asian populations as having a combination of eastern and western anthropometric traits (Bowles 1977). The analysis of classical genetic markers, on the other hand, has largely ignored Central Asia, and has not expanded on the idea that Central Asia is intermediate between Europe and Asia (Cavalli-Sforza and Bodmer 1999; Cavalli-Sforza et al. 1994; Comas et al. 1998). The

current consensus is that the inhabitants of Central Asia are the result of admixture between differentiated gene pools from Europe and East Asia (Calafell et al. 2000; Comas et al. 1998; Comas et al. 2004; Wells et al. 2001); however, the age of this admixture has not been well estimated nor have the processes that may have shaped genetic variation in this region been well explained.

MtDNA Studies in Central Asia

Thus far, the genetic research that has been done in Central Asia utilizing mtDNA has demonstrated that Central Asian populations exhibit a high degree of genetic diversity (Calafell et al. 2000; Chaix et al. 2008; Comas et al. 1998; Comas et al. 2004). Two explanations have been put forward to account for this diversity: 1) Central Asian populations represent an incubation phase of Eurasian genetic variation prior to a split toward east and west or 2) the high diversity present in Central Asia is the result of admixture between differentiated east and west Eurasian populations (Calafell et al. 2000; Chaix et al. 2008; Comas et al. 1998; Comas et al. 2004). Much of the research investigating this question has utilized uniparentally inherited Y chromosome and/or mitochondrial DNA (e.g., Quintana-Murci et al. 2004; Wells et al. 2001). MtDNA studies suggest that Central Asia has been a melting pot of diversity from east and west, creating a high amount of genetic variation (Calafell et al. 2000; Comas et al. 1998; Comas et al. 2004; Quintana-Murci et al. 2004).

Comas and colleagues (1998, 2004) have suggested that the diversity in Central Asia is the result of extensive admixture between Europeans and East Asians in Central

Asia. This gene flow would have been heightened during the Silk Road trade and had to have occurred after the divergence of eastern and western Eurasian human groups (Comas et al. 1998; Comas et al. 2004). This implies that it had to have happened fairly recently; although, a date for this admixture is not directly estimated. In 2004, Comas et al. identified two mtDNA haplogroups, D4c and G2a, that date to around 30-25,000 years ago and may represent a portion of the gene pool that can be regarded as Central Asian specific. These two mtDNA haplogroups might reflect the remnants of the first peopling by early humans; although, the authors suggest that they are most likely reflective of haplogroups that originated in East Asia and then expanded in Central Asia (Comas et al. 2004). The frequency and distribution of these haplogroups in Central Asian populations needs to be further investigated.

In a broader examination of genetic variation, Quintana-Murci et al. (2004) analyzed mtDNA from 23 populations from the southwestern Asian corridor and their results confirm those of Comas et al. (1998, 2004). Central Asian populations were found to have substantial portions of lineages from western Eurasia, eastern Eurasia, and South Asia. Additionally, the highest mtDNA variation is seen in populations from the Indus Valley and Central Asia. This finding suggests that this region is where western Eurasian lineages meet up with Eastern Eurasian and South Asian genetic branches. The authors suggest that high levels of genetic variation in this region may be the result of continuous, successive migrations from diverse geographic sources throughout different time periods. However, only Uzbeks and Turkmen were included in the Central Asian sample.

Yao et al. (2004) sequenced the HVS-I region of the mitochondrial genome from six populations (Han, Hui, Kazakh, Mongolian, Uyghur, and Uzbek) from Xinjiang, China. The authors were interested in further testing the competing hypotheses regarding Central Asian origins. Their findings were consistent with those of Comas et al. (1998), Calafell et al. (2000), and others, suggesting that the mtDNA variation present in Central Asia is the result of genetic admixture. The extent of that admixture was shown to vary in the populations from Xinjiang with Kazakhs, Uyghurs, and Uzbeks showing the highest frequency of west Eurasian-specific haplogroups. Additionally, the Uyghur and Uzbek populations seem to have experienced more gene flow than the Kazakhs.

While the previous study, used the HVS-I region of mtDNA, Irwin et al. (2010) sequenced the complete mitochondrial control region of 1,575 residents of Uzbekistan. Along with Uzbek individuals, the authors obtained samples from other ethnic groups including Afghans, Kazakhs, Kyrgyz, Tajiks, and Turkmen. The results of this study show that the different subpopulations of Uzbeks in Uzbekistan do not differ significantly in mtDNA, but there are detectable differences between Uzbeks and individuals with ancestry from neighboring areas. This finding further cements the idea that there is a high degree of genetic diversity present in Central Asian populations.

Although the dates of the proposed admixture in Central Asia have not been estimated, Lalueza-Fox et al. (2004) used 36 teeth from prehistoric sites throughout Kazakhstan to generate HVS-1 sequences. The results of this study showed that the mitochondrial haplogroup composition of the sample after the seventh century BCE is comparable to modern Kazakhs. However, there were some differences detected

between modern Kazakhs and the sample prior to the seventh century BCE. There is a general absence of east Eurasian sequences in the sample dating prior to the 7th century BCE. This is suggested to be because of a prior expansion into Central Asia from the west, perhaps related to the Tarim Basin mummies (Lalueza-Fox et al. 2004). Additionally, an interesting finding is the presence in "the ancient sample of sequences from Central Asia that are mainly distributed far into the West, such as the Caucasus and central Mediterranean areas" (Lalueza-Fox et al. 2014: 945).

The main takeaway from mtDNA analyses in Central Asia is that the levels of genetic diversity present in the region are high, and the modern gene pool appears to be composed of matrilineal lineages from East and West Eurasia, primarily (Comas et al. 1998; Comas et al. 2004; Irwin et al. 2010; Quintana-Murci et al. 2004; Yao et al. 2004). The current consensus is that this high genetic diversity and the presence of a large number of mtDNA sequences originating outside Central Asia is the result of admixture between differentiated gene pools from East and West Eurasia.

Y chromosome Studies in Central Asia

As compared to mtDNA studies, research using the Y chromosome has had somewhat conflicting results. Analyses based on Y chromosome data support the idea that Central Asian populations are one of the oldest in Eurasia (Wells et al. 2001), but were also recipients of migrations (Zerjal et al. 2002). Wells et al. (2001) found that Central Asian populations are one of the oldest on the Eurasian continent and the high diversity in Y-chromosomal DNA supports an early settlement of Central Asia sometime

between 40-50,000 years ago. This appears to contradict the results from mtDNA analyses, which have not been interpreted as suggestive of an ancient origin for Central Asians (Comas et al. 1998; Comas et al. 2004; Quintana-Murci et al. 2004). However, these results are not necessarily contradictory and may simply reflect different sex-based migration patterns in Central Asia. Additionally, an east-west clinal pattern has been identified in the Y chromosome (Zerjal et al. 2002). This pattern was interpreted as the result of the ancient peopling of this region and has been reinforced by subsequent migrations; however, a clear overall pattern has not been identified (Zerjal et al. 2002).

Genetic analyses of the Y chromosome in Central Asia have also been used to examine questions of the effects of cultural customs on genetic variation (Chaix et al. 2008; Chaix et al. 2004; Chaix et al. 2007). Chaix et al. (2004) studied Y chromosome variation in five different patrilineal populations from Central Asia: Kazakhs, Turkmen, Karakalpaks Qongirat, Uzbeks, and Karakalpaks On Tort Uruw. The authors were investigating whether descent-group organization in patrilineal societies was detectable in the Y chromosome. The results indicate that individuals from the same lineage and clan share a recent common ancestor, but at the tribal level this is not the case. Chaix et al. (2004) conclude that tribes are therefore a collection of clans who invented a mythical ancestor as a way of strengthening group unity. One interesting finding was that the Uzbek sample did not have a high kinship coefficient at any level – lineage, clan, or tribe. This demonstrates how variation in lifestyles can explain heterogeneity in social structure.

Dulik et al. (2011) investigated the population history of Altaian Kazakhs using 60 biallelic markers and 17 STRs from the NRY. There were differences detected among various groups of Altaian Kazakhs, and these differences are attributed to the way they arrived in the Altai-Sayan region. Assessments of Altaian Kazakhs and indigenous Kazakhs show that they have a shared biological history. Additionally, the mtDNA data suggest that Altaian Kazakhs come from a common gene pool, but the Y chromosome data show that Kazakhs and Mongolians diverge from other groups in Central Asia. Ultimately, the shared paternal ancestry of Kazakhs separates them from other populations from Central Asia. The authors conclude that the cultural traditions of the Kazakhs influenced their present pattern of genetic variation.

Balaresque et al. (2015) surveyed 5321 Y chromosomes from 127 Asian populations to investigate whether lineage expansions could be identified. Two instances of successful Y-lineages have been identified in Asia previously, one from Genghis Khan and the other Giocangga. The authors identified 11 descent clusters that indicate historic examples of high male reproductive success. The successful lineages with recent origins are found almost exclusively in Turkic-speaking pastoral nomadic groups. The authors suggest that this may reflect a shift in political organization.

The conflicting findings of research utilizing mtDNA and the Y chromosome leave the question of the explanation for the high genetic diversity in Central Asia unresolved.

Multilocus Studies in Central Asia

There have been a variety of multilocus studies on the genetic variation in Central Asia. Most of this research has combined data from both mtDNA and the Y chromosome (Calafell et al. 2000; Chaix et al. 2008; Chaix et al. 2007). Calafell et al. (2000) analyzed the mtDNA hypervariable region I and seven microsatellites in the non-recombining segment of the Y chromosome in samples from three Central Asian populations: Kazakhs, Kyrgyz, and Uyghurs. The results of this study indicate that Central Asian populations have an admixed origin. In addition, traces of the colonization of high altitudes were detected in the Y-chromosome; while a higher female migration rate as the result of patrilocal customs was indicated by the mtDNA sequences.

Chaix et al. (2007) investigated the effects of different lifestyles and social organization on genetic diversity. The HVS-I portion of the mitochondrial DNA along with 6 STRs from the nonrecombining portion of the Y chromosome from pastoral and farming societies were used in this study. The findings indicate that pastoralists have had a significant loss of diversity in the Y-chromosome when compared to farmers, but no such differences were detected in the mtDNA. The authors attribute this result to the dynamics of patrilineal descent groups, and suggest that the observed genetic patterns are the result of social organization.

Chaix et al. (2008) investigated the pattern of population expansions in Eurasia using the HVS-I segment of the mitochondrial DNA and 7 STRs from the nonrecombining portion of the Y chromosome. The results of this study show that there is a decrease in expansion ages from east to west across Eurasia; this is supported by

both the mtDNA sequences and the Y chromosome data. The authors suggest that these results support the spread of genetic diversity from the Far East into Central Asia and subsequently into Europe. Thus, Central Asia is neither an incubator nor completely the result of admixture, but likely served both roles at different time periods. The authors postulate that this spread of genetic diversity from east to west might have come about as the result of migration(s) associated with the Aurignacian culture (Chaix et al. 2008).

Heyer et al. (2009) used mitochondrial and Y chromosome data from Central Asian populations to try to understand their origins better by utilizing a larger sample size and more representation within Central Asia. Additionally, the authors were interested in assessing how ethnicity plays a role in the patterning of genetic differences. The results of this study show that for the Y chromosome there are more differences between populations of the same ethnic groups, while the converse is seen for the mtDNA in the Turkic group. A minimal age of these ethnic groups is calculated and is much higher than that based on historical records for two of the groups. This lends support to the idea that ethnicity, for at least two of the groups, should be viewed as "a constructed social system maintaining genetic boundaries with other ethnic groups, rather than the outcome of common genetic ancestry" (Heyer et al. 2009: 49).

Heyer et al. (2015) investigated the extent to which social organization impacts patterns of genetic diversity. They used mtDNA and Y chromosome polymorphisms of patrilineal and cognatic Central Asian populations. The results indicate that in patrilineal societies there is a male-biased transmission of reproductive success. The authors also found a higher paternal fertility transmission in patrilineal societies versus cognatic

groups. This result might be a factor contributing to the lower intra-population genetic variation and higher genetic diversity among patrilineal populations.

A limited amount of research has been done in Central Asia utilizing autosomal microsatellites or single nucleotide polymorphisms (SNPs). The research that has been done utilizing nuclear DNA has focused on examining the question of sex-specific population structure (Segurel et al. 2008) or the distribution of population specific markers like those for diabetes type 2 (Segurel et al. 2013) or lactase persistence (Heyer et al. 2011). There is one notable exception, the research by Martinez-Cruz et al. (2010). Their study utilized 27 autosomal microsatellite loci and found that Central Asian genetic variation is primarily shaped by language. In addition, their results suggest that the genetic landscape of Central Asia is the result of the historical movement of eastern Turkic-speaking groups (Martinez-Cruz et al. 2010). Lastly, the recurrent expansions of eastern nomadic groups do not appear to have resulted in the replacement of local groups, but partial admixture instead (Martinez-Cruz et al. 2010).

Application to this Study

This review of the current state of genetics research in Central Asia has shown that the question of Central Asian origins and time depth remains. Studies from both mtDNA and the Y chromosome have indicated that there is a high degree of genetic diversity present in Central Asia, but this variation has been interpreted in conflicting ways. The results from mtDNA analyses are interpreted as supporting admixture between differentiated east and west gene pools as an explanation, while the results from

Y chromosome studies suggest that Central Asians have an ancient origin (Calafell et al. 2000; Comas et al. 1998; Comas et al. 2004; Quintana-Murci et al. 2004; Wells et al. 2001; Zerjal et al. 2002).

Research up to this point has not fully elucidated the distribution of genetic variation in Central Asia. As demonstrated above, much of the research on Central Asia has not focused on answering questions about the population structure of Central Asian populations and how this structure has been influenced by population history or geographic barriers or conduits. The research done in this area has shown that there is a difference in the genetic variation in mtDNA versus the Y chromosome, and so this is something that must be kept in mind, especially as the present study uses mtDNA. This study seeks to answer questions about the patterning of genetic variation in Central Asia by examining mtDNA haplogroup frequency and distribution, as well as measures of genetic diversity. Additionally, the present study is the largest such study of its kind for this region; in terms of both the Central Asian sample, as well as the comparative sample.

CHAPTER IV

THEORETICAL FRAMEWORK: POPULATION STRUCTURE AND HISTORY

The theoretical framework for this research comes from the field of anthropological genetics and examinations of human variation using genetic data. As such, I will describe what population structure and history are and how they have been studied in anthropological research using genetic data. Finally, I will explain how this theoretical framework is the foundation upon which the current research on Central Asian population structure and history has been built.

What is Population Structure?

The current research examines population structure in Central Asia, specifically the distribution of genetic variation within and between populations in this region. The null hypothesis for populations is that they are unstructured; that is, populations are panmictic or mating randomly (Wright 1921). This is the assumption in theoretical random models (Kimura 1953; Wright 1921; Wright 1943). However, this is not a reasonable assumption for human populations or, in fact, any species (Fix 1999; Hartl and Clark 1997; Templeton 2006). Almost universally among species, some sort of geographic structuring exists; in other words, a non-random pattern in the spatial distribution of organisms (Hartl and Clark 1997; Repaci et al. 2007). Therefore, the typical assumption for human populations is that they will be structured following an isolation-by-distance model. In this model, gene flow is spatially restricted across a

continuously distributed population such that geographically closer groups are more similar and those that are further apart are more different (Wright 1943). Thus, random mating is limited by distance such that individuals are more likely to mate with neighbors than with those farther away (Fix 1999).

Kimura and Weiss (1964) proposed the stepping-stone model, a refinement to the isolation-by distance model, that more closely approximates many natural populations including humans (Athreya 2006; Fix 1999; Kimura and Weiss 1964). The stepping-stone model of population structure says that a whole population is subdivided into local groups and within each group mating occurs at random. An exchange of individuals between groups is allowed to occur, but only between adjacent subpopulations (Athreya 2006; Fix 1999; Kimura 1953).

A significant correlation between genetic variation and geographic distance is expected according to the isolation-by-distance model (Crow and Kimura 1970; Malécot 1969; Morton 1973) and "geographic distance is most often a significant and frequently primary determinant of genetic variation between populations within a relatively small geographic region" (Relethford 2004:500). However, there are a number of possible departures that are possible from this "ideal" population structure. These departures may be caused by random genetic drift, natural selection, population extinctions and recolonizations, gene flow, and unequal population sizes (Relethford 1983; Relethford and Harpending 1994).

One of the principal genetic consequences of population structure is a reduction in heterozygosity (average proportion of heterozygous genotypes) relative to that

anticipated under random mating (Wright 1969). A reduction in heterozygosity because of population structure means that within subdivided populations there will be an increase in homozygosity or the average proportion of homozygous genotypes (Templeton 2006). The effect of population structure on genetic variation is to increase variation between populations and decrease variation within populations typically, but this is system of mating dependent (Spuhler 1973; Templeton 2006; Wright 1969). There a number of situations that might result in a misleading picture of the structure of a population including variation in levels of gene flow, the presence of selective clines, and balancing selection (Muirhead 2001; Relethford 2004; Wright 1939). For example, in studies that assume an isolation-by-distance model, long-range migration is considered a constant, but on a global scale it might vary across geographic space. In other words, the probability of long-range migration decreases at a predictable rate with distance (Relethford 2004).

Another possible scenario for confusion would be a case where the formation of selective clines might mimic the pattern that is expected under an isolation-by-distance model (Relethford 2004). In the case of selection, selective forces might be acting on different genetic loci in divergent ways as well (Segurel et al. 2012). Additionally, uniparentally inherited versus diploid loci might show different patterns of genetic variation as the result of sex-specific migration patterns like would result if patrilocality, post-marital residence with the husband's group, is practiced (Chaix et al. 2007; Segurel et al. 2008). Because of these confounding factors we might see a difference in the

structure inferred from different DNA types such as mtDNA, Y-chromosome haplotypes, or different autosomal loci.

Anthropologists have been interested in examining population structure for many years (Allison et al. 1956; Boyd 1963; Crawford and Leyshon 1971; Salzano 1968; Sukernik et al. 1977; Williams-Blangero and Blangero 1989; Workman et al. 1973; Workman and Niswander 1970). Anthropological research on population structure has used both morphological and genetic data and has examined morphological and genetic variation in fossil hominin species as well as modern humans (Athreya 2006; Athreya 2009; Gonzalez-Jose et al. 2004; Relethford 1994; Relethford and Harpending 1994; Relethford et al. 1980; Roseman 2004; Roseman 2016; Underhill and Kivisild 2007; Wang et al. 2000; Yao et al. 2004). Additionally, population structure has been studied at the local (Cavalli-Sforza 1969; Chu et al. 1998; Derenko et al. 2000; Malyarchuk et al. 2010a; Relethford and Crawford 2013), regional (Martinez-Cruz et al. 2010; Quintana-Murci et al. 2004; Reich et al. 2009; Simoni et al. 2000; Wells et al. 2001), and global levels (Cavalli-Sforza et al. 1994; Hammer et al. 2001; Kumar et al. 2006; Relethford 2004; Rosenberg et al. 2002).

An examination of population structure is particularly relevant to the present study for two main reasons. First, knowledge of patterns of genetic variation at a regional or global level allow for attempts to understand the origin and migration of populations (Calafell et al. 2000; Comas et al. 1998; Hodoglugil and Mahley 2012; Martinez-Cruz et al. 2010). Central Asia has largely been ignored in studies of global population structure and, as a result, there is currently an incomplete understanding of

models of global human variation. Second, it is incredibly useful to attempt to account for the effects of population structure on genetic variation to try to get a better understanding of the history of a population or group of populations (Hanihara and Ishida 2009; North et al. 2000; Relethford 1996; Relethford and Crawford 2013; Templeton 2003). Population structure has been examined to a certain degree in Central Asia, but there are issues with these analyses including scope, lack of a representative sample of Central Asian populations, and/or a small comparative sample (Calafell et al. 2000; Chaix et al. 2007; Comas et al. 1998; Comas et al. 2004).

In this study, the primary question regarding population structure is whether it is geographically structured and if so, what does the distribution of genetic variation demonstrate about the history of interactions between populations in Central Asia?

What is Population History?

In addition to examining population structure, the current research also examines questions relating to the population history of Central Asia and its effect on the current patterns of human genetic variation. Central Asia has a complex history including internal and external takeovers, culturally diverse interactions as the result of trade along the Silk Road, and a variety of cultural traditions including patrilocality that can have an influence on patterns of genetic variation.

Population history is concerned with past events (evolutionary and historical) and their timing, which may have impacted the current genetic makeup of populations (Relethford 2012; Rubicz et al. 2007; Templeton 1998). It can be difficult to tease apart

the effects of population history and population structure, and a similarity between gene frequencies may be a reflection of common ancestry or it may have been influenced by evolutionary forces, historical events, and/or mate exchange (Harpending and Jenkins 1973; Templeton et al. 1995). That being said, population history typically deals with the level of similarity between populations that is the result of common ancestry and/or gene flow (Relethford 1994; Relethford 1996; Relethford and Harpending 1994). As such, it is concerned more with how historical events, like culture contact or population movements, have influenced patterns of genetic variation between populations (Relethford 2012).

Population history generally concentrates on the genetic impact of factors, such as invasions, migrations, and other events that affect genetic exchange between populations, on genetic distances between a set of populations (Mielke et al. 2006). The primary goal of the analysis of genetic variation is often the reconstruction of population history; ranging from the analysis of local and regional groups (Barbujani and Bertorelle 2001; Capelli et al. 2001; Reich et al. 2009; Relethford and Crawford 1995; Relethford and Crawford 2013) , to studies of global population history (Cavalli-Sforza and Bodmer 1971; Cavalli-Sforza et al. 1993), to the examination of the genetic history of *Homo sapiens* (Relethford 1996; Sokal et al. 1997). At its most basic level, genetic variation between populations can be seen as indicative of genetic drift, gene flow, and common ancestry; therefore, it is important to understand what blend of these is responsible for the observed distribution of genetic variation (Relethford 1996).

Studies of population history in anthropology date back to at least the 1950s, with the pioneering work of Hanna et al. (1953) on the Pima Indians. More recent research includes the examination of the origins of different local and regional populations (Mielke et al. 1994; Reich et al. 2012; Relethford and Crawford 1995; Relethford and Crawford 2013; Torroni et al. 1994). This includes research that has been done on the peopling of Europe, Oceania, and the Americas (Achilli et al. 2013; Arredi et al. 2007; Matisoo-Smith 2007; Szathmary 1993).

Current research on population history in Central Asia has failed to utilize a broad anthropological perspective (Calafell et al. 2000; Comas et al. 1998; Wells et al. 2001; Zerjal et al. 2002). In contrast, the present study uses a holistic approach that includes knowledge of the cultures, evolution, and history of the populations in this region. This research fits into the theoretical framework of population history by examining the effects of evolutionary as well as historical events on the patterns of genetic variation observed between populations in Central Asia as well as neighboring populations.

Application to this Study

This overview of population history and structure and the discussion of their application in anthropological studies shows why both are necessary in order to gain a better understanding of patterns of human genetic variation in Central Asia. The research presented here answers the following questions regarding population history and structure in Central Asia:

Q1: How is genetic variation patterned in Central Asia?

Genetic research in Central Asia has shown that populations from this region exhibit a high degree of genetic diversity (Chaix et al. 2008; Comas et al. 1998; Comas et al. 2004; Hammer et al. 2001; Wells et al. 2001; Zerjal et al. 2002). However, the pattern of this genetic variation, i.e., the population structure, has not been fully explained. Research using the Y chromosome has recognized an east-west clinal pattern (Zerjal et al. 2002), while autosomal DNA analyses (Martinez-Cruz et al. 2010; Segurel et al. 2008) did not find evidence of a correlation between geographic distance and genetic variation. Martinez-Cruz et al. (2010) did find that Central Asian genetic diversity was shaped by linguistic affiliation. The current study seeks to explain the pattern of genetic diversity in Central Asia by investigating not only the question of geographic structure, but also including an examination of population history.

Q2: What, if any, geographic barriers have or continue to affect population interactions in Central Asia?

There are a number of geographic barriers in Central Asia that have the potential to affect population movements. These include the Altai Mountains, Caspian Sea, Himalaya Mountains, and Ural Mountains. Because Central Asia has largely been ignored in studies of global human genetic variation, it is not clear whether genetic variation in Central Asia is distributed following an isolation by distance model or whether geographic barriers have affected the current population structure in this region. Although previous research has not identified a correlation between geographic distance

and genetic variation (Martinez-Cruz et al. 2010; Segurel et al. 2008), this question bears further inquiry, especially in light of the unique location of Central Asian populations.

Q3: How has population history influenced the distribution of genetic variation that is seen in modern-day Central Asian populations?

The history of Central Asia is complex and there have been a large number of population movements within and through the region (see Chapter II). It is not possible to understand the population structure of Central Asia without taking this population history into account. Because of its multifaceted history, there are several questions that can be asked regarding the effects of population history on genetic variation in this region. This study focuses on three: 1) Have Indo-European-speaking groups (Tajiks) been replaced by Turkic-speaking groups (Kazakhs, Kyrgyz, Turkmen, and Uzbeks) throughout Central Asia as has been suggested by historical records?; 2) Are Kazakhs and Uzbeks more genetically similar to one another than either is to other Turkic-speaking populations because they became distinct ethnic groups only within the last 500+ years?; and 3) Did the process of "Russification" described as being more prominent among Kazakhs leave any traces in the mtDNA of modern-day Kazakhs?

CHAPTER V

MATERIALS

In this chapter, I discuss the genetic sample included in this study. The selection process for inclusion is outlined, and the division of the sample is discussed.

MtDNA Sample

To examine the population structure and history of Central Asia, I assembled a sample of mtDNA control region sequences downloaded from GenBank (Table 1). The mtDNA sequences were found by first reviewing the literature to locate accession numbers, and then searching GenBank directly using accession numbers when possible, if not geographic locations, author names, and populations were used. The sample of mtDNA sequences compiled for this study was based on the following criteria: a) geographic location, b) availability for download, and c) sequence at least 90% complete.

The main criterion for inclusion in this study, besides availability, was that the genetic sample came from one of the target areas: Caucasus North, Caucasus South, Central Asia, East Asia, East Europe, Near East, North/Central Asia, North/East Asia, North Asia, South/Central Asia, and South Asia. These regional subdivisions are based on conventional geography and groupings used in the literature (Chaix et al. 2008; Derenko et al. 2014; Pala et al. 2012). Because I used publicly available mtDNA sequences there is a lack of consistency as far as labeling. For example, some samples

are listed by country, while others are listed by cultural labels. In some cases, like the Adygei for example, I maintained the cultural label, but still grouped based on geography. Based on this, the mtDNA samples were divided into the aforementioned 11 groups.

TABLE 1. *MtDNA Control Regions Sampled in the Present Study*

Region	Population/Location	Map ID	N
Caucasus North	Adygei (SW Russia)	1	4
	Dargin (S Russia)	2	3
	North Ossetian (S Russia)	3	14
Caucasus South	Armenia	4	20
	Azerbaijan	5	20
	Georgia	6	20
Central Asia	Kazakhstan	7	256
	Kyrgyzstan	8	249
	Tajikistan	9	244
	Turkmenistan	10	249
	Uzbekistan	11	328
East Asia	Bargut (NE Inner Mongolia)	12	20
	Chinese (Hong Kong)	13	377
	Han (China, Taiwan)	14	16
	Mongolia	15	9
East Europe	Albania	16	5
	Belarus	17	20
	Bosnia	18	5
	Bulgaria	19	20
	Chuvash (central Russia)	20	4
	Csango (Romania)	21	100
	Czech Republic	22	20
	Estonia	23	7
	Hungary	24	211
	Lithuania	25	12
	Kalmyk (SW Russia)	26	6
	Moldova	27	4
	Poland	28	20

TABLE 1. *continued*

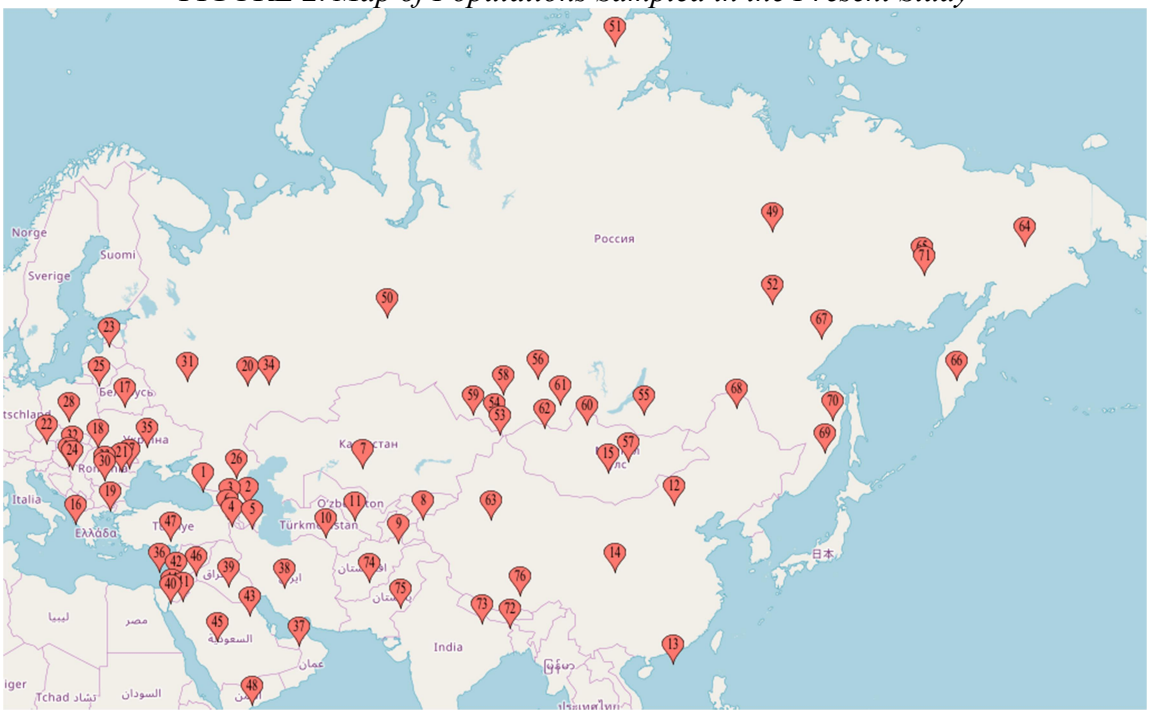
Region	Population/Location	Map ID	N
East Europe (con't)	Roma (Hungary)	29	205
	Romania	30	17
	Russia	31	151
	Slovakia	32	20
	Szekely	33	178
	Tatars (Volga) (W Russia)	34	20
	Ukraine	35	20
Near East	Cyprus	36	91
	Dubai (UAE)	37	12
	Iran	38	20
	Iraq	39	182
	Israel	40	16
	Jordan	41	12
	Lebanon	42	20
	Kuwait	43	381
	Palestine	44	9
	Saudi Arabia	45	18
	Syria	46	6
	Turkey	47	20
	Yemen	48	19
North Asia	Evenki (N Siberia)	49	19
	Mansi (NW Siberia)	50	12
	Nganasan (N Siberia)	51	12
	Yakut (NE Siberia)	52	11
North/Central Asia	Altaian Kazakh (S Siberia)	53	13
	Altaian Kizhi (S Siberia)	54	20
	Buryat (Siberia)	55	20
	Ket (central Siberia)	56	4
	Khamnigan (S Siberia)	57	20
	Shor (SW Siberia)	58	12
	Teleut (SW Siberia)	59	8
	Tofalar (S Siberia)	60	4
	Tubular (S Siberia)	61	20
	Tuvinian (S Siberia)	62	17
	Uyghur (W China)	63	2
North/East Asia	Chukchi (Far East Russia)	64	20
	Even (Far East Russia)	65	13
	Koryak (Far East Russia)	66	19
	Negidal (Far East Russia)	67	6
	Nivkhi (Far East Russia)	68	20

TABLE 1. *continued*

Region	Population/Location	Map ID	N
North/East Asia (con't)	Udegey (Far East Russia)	69	20
	Ulchi (Far East Russia)	70	14
	Yukaghir (NE Siberia)	71	20
South Asia	India	72	20
	Nepal	73	40
South/Central Asia	Afghanistan	74	98
	Pakistan	75	5
	Tibet	76	20
			4169

For all populations sampled (Table 1), I tried to include a minimum of 20 mtDNA sequences, but in some cases this was not possible. In total, I assembled a sample of 4,169 mitochondrial control regions from 76 populations. The populations sampled and sample size is seen in Table 1 and the geographic location of all samples is seen in Figure 2. I have also included a complete list of all mtDNA sequences downloaded along with GenBank accession numbers and references in Appendix A. For each geographic region, I will provide more specific information on the sample composition and include a description of the geographic location and history of each population.

FIGURE 2. *Map of Populations Sampled in the Present Study*



(Map data created by ©2018 OpenStreetMap contributors, Open Database License v 1.0)

Caucasus North

Samples from three populations in this region were collected including: Adygei, Dargin, and North Ossetian (Table 2). Table 2 includes the sample size, the references from which the samples were collected, and the label(s) given by the researchers who submitted the sequences to GenBank.

Adygei

The Adygei, also known as Circassians or Adyghes, live mostly in southwestern Russia, particularly in the republics of Adygea, Kabardino-Balkaria, and Karachay-Cherkessia (Danver 2013). The Adygei homeland was the location of the Bronze Age

Kurgan culture, today classified with the Proto-Indo-Europeans. Some researchers postulate that the ancestors of the Adygei may themselves have participated in the Kurgan culture. Whether or not that is the case, the Adygei have been in or near the northern Caucasus area for millennia (Danver 2013; Khanam 2005).

Dargin

The Dargin originate in the northern Caucasus region. They make up the second largest ethnic group in Dagestan, a Russian republic in the southernmost part of Russia, bordered to the east by the Caspian Sea. Traditionally, they were herders, primarily of sheep, and were known for their goldsmith skills (MacKenzie 2005). They speak Dargwa, a North Caucasian language (Dalby 2004). The Dargin have been under Russian rule since the 19th-century (MacKenzie 2005).

North Ossetians

Ossetians are an Iranic people living in the Central Caucasus region. They are divided politically between states in northern Georgia and southern Russia. Most Ossetians live in the Republic of North Ossetia-Alania, a federal subject of Russia; hence, the name North Ossetians (Danver 2013). The ancestors of the Ossetians are Scythian tribes that migrated from the Eurasian steppe to the Caucasus Mountains around 200 B.C.E. The Scythian had Iranian origins, and this affiliation is kept in the name Iron, which is what eastern Ossetians call themselves (Danver 2013; De Waal 2010).

TABLE 2. *Caucasus North Sample Composition*

Population/Location	N	Reference	Label/Collection Location
Adygei	4	Achilli et al. (2005)	Adygei
Dargin	3	Roostalu et al. (2007)	Dargin
North Ossetian	3	Pala et al. (2012)	Russia: North Ossetia-Alania Republic
	1	Pennarun et al. (2012)	Ossetia
	1	Roostalu et al. (2007)	North Ossetian #71
	7	Fernandes et al. (2012)	Russia: North Ossetia
	2	Pala et al. (2012)	Russia: Ossetia
	21		

Caucasus South

Samples from three countries were collected and include: Armenia, Azerbaijan, and Georgia (Table 3). Table 3 includes the sample size, the references from which the samples were collected, and the label(s) given by the researchers who submitted the sequences to GenBank.

Armenians

Armenia is located in the South Caucasus region of Eurasia. It is bordered by Georgia to the north, Turkey to the west, Azerbaijan to the east, and Nakhichevan to the south (Hewsen and Salvatico 2001). Armenians, who call themselves Hayk, most likely originated in the Southern Caucasus region, the area that straddles the border between Eastern Europe and Southwest Asia (Chahin 2001; Danver 2013). More than 3,500 years ago, the ancestors of modern Armenians migrated to modern-day Armenia; although, most Armenians today live outside their historical homeland. Armenians have Indo-

European origins and consider themselves distinct from the indigenous peoples of the Caucasus region (Danver 2013).

Azerbaijanis

Azerbaijan is located in the South Caucasus region, at the crossroads between Southwest Asia and Southeastern Europe. Azerbaijan is bordered to the east by the Caspian Sea, to the north by Russia, to the northwest by Georgia, by Armenia to the west, and Iran to the south (Aliprandini 2017a). The Azeri, or Azerbaijanis, have lived in the modern-day Republic of Azerbaijan since the early Middle Ages. The ancestors of the Azeri were Turkic tribes who migrated to the southern Caucasus region from southern Siberia. However, the Azeri ethnicity emerged on the periphery of Europe more than 1,000 years ago (Altstadt 1992). The Azeri population is divided geographically into two main groups – the northern group is located mainly in Azerbaijan and the southern group is the largest minority in Iran (Danver 2013).

Georgians

Georgians call themselves *kartv-el-I*, or Kartvelians (Danver 2013). They are indigenous to the Caucasus region of Central Europe. Today, Georgians reside in the western and southern areas of the Caucasus Mountains, primarily in the country of Georgia (Mądry and Kaczmarek Khubnaia 2016). Georgia is bordered to the north by Russia, by the Black Sea to the west, by Turkey and Armenia to the south, and by Azerbaijan to the southeast. Culturally, Georgians are distinguished from other peoples of the Caucasus because they are Orthodox Christians (Danver 2013; Sullivan 2003).

TABLE 3. *Caucasus South Sample Composition*

Population/Location	N	Reference	Label/Collection Location
Armenia	30	Schonberg et al. (2011)	Yerevan, Armenia
	11	Pala et al. (2012)	Armenian
	1	Roostalu et al. (2007)	Armenian #2
	1	Kushniarevich et al. (2013)	Armenia
	1	Pennarun et al. (2012)	Armenia
Azerbaijan	30	Schonberg et al. (2011)	Baku, Azerbaijan
	6	Pala et al. (2012)	Azerbaijan
	3	Fernandes et al. (2012)	Azerbaijan
Georgia	2	Pala et al. (2012)	Georgia
	28	Schonberg et al. (2011)	Batumi, Georgia
	1	Ingman et al. (2000)	From Georgian individual
	1	Kivisild et al. (2006)	Georgia
	2	Achilli et al. (2004)	Georgia
	1	Pennarun et al. (2012)	Georgia
	1	Ennafaa et al. (2009)	Georgia
	1	González et al. (2007)	Georgia
	60		

Central Asia

The populations sampled for this region include: Kazakhstan, Kyrgyzstan, Tajikistan, Turkmenistan, and Uzbekistan (Table 4). Table 4 includes the sample size, the references from which the samples were collected, and the label(s) given by the researchers who submitted the sequences to GenBank.

Kazakhs

Kazakhs are a Turkish people from Central Asia with significant Mongolian, Persian, and Russian influences. They reside in their historical homeland in the nation of Kazakhstan, which is south of Russia and west of Mongolia (Danver 2013). Kazakhs emerged as a unique ethnic group sometime between the 14th- and 16th-centuries on the

Central Asian steppes in the area of Zhetisu, around the modern city of Almaty in southeast Kazakhstan. The Kazakh khanate was founded in 1466, which marks the year of their independence from the Uzbeks, a related Turkic group (Danver 2013; Weller 2006).

Kyrgyz

Today, most Kyrgyz live in the nation of Kyrgyzstan, positioned between China, Kazakhstan, Tajikistan, and Uzbekistan. The Kyrgyz are a Turkic people with a Central Asian nomadic heritage and significant influences from Mongolians, Persians, and Russians (Danver 2013). Modern-day Kyrgyz are descendants of the Yenisei Kyrgyz, who originally lived along the Yenisei River in Siberia. Most Kyrgyz migrated to present-day Kyrgyzstan between the 9th- and 12th-centuries (Abazov 2008; Danver 2013).

Tajiks

The Tajiks have Persian heritage and their history, culture, and language are entwined with those of Afghans, Iranians, Russians, and Uzbeks (Danver 2013). Traditionally, they have been sedentary in contrast to other Central Asian peoples (Abazov 2007). Today, Tajiks live in their historical homeland in the country of Tajikistan, which is situated between Afghanistan and Pakistan to the south, Uzbekistan to the west, Kyrgyzstan to the north, and China to the east (Abazov 2008).

Turkmen

Traditionally, all of the Western or Oghuz Turks were called Turkmen; however, the term Turkmen, today, refers only to the Turkic people who live primarily in

Turkmenistan, but also in Afghanistan, Iraq, and Syria (Danver 2013). Turkmenistan is located in Central Asia and is bordered by Afghanistan, Iran, Kazakhstan, and Uzbekistan, as well as the Caspian Sea (Aliprandini 2017b). For much of their history, Turkmen were nomadic and settled into sedentary life only in the early 20th-century (Edgar 2004).

Uzbek

The name Uzbek was mentioned for the first time in Persian historical chronicles, and was used to represent the "wild tribes" north of Persia (Danver 2013). The ethnic origins of the Uzbek are still questioned as discussed in Chapter 2, but what is known is that until the Russian conquest of the region in the 19th-century, the Uzbek were made up of different groups characterized by permanent rivalries among tribal clans in the steppes and deserts of Central Asia (Sengupta 2003). Today, Uzbeks live primarily in the Republic of Uzbekistan, a country in Central Asia bounded by Afghanistan, Kazakhstan, Kyrgyzstan, Tajikistan, and Turkmenistan (Danver 2013).

TABLE 4. *Central Asia Sample Composition*

Population/Location	N	Reference	Label/Collection Location
Kazakhstan	256	Irwin et al. (2010)	Ind w/ ancestry Kazakhstan
Kyrgyzstan	249	Irwin et al. (2010)	Ind w/ ancestry Kyrgyzstan
Tajikistan	244	Irwin et al. (2010)	Ind w/ ancestry Tajikistan
Turkmenistan	249	Irwin et al. (2010)	Ind w/ ancestry Turkmenistan
Uzbekistan	328	Irwin et al. (2010)	Individual of Uzbek ancestry
	1326		

East Asia

In this geographic region, four populations were sampled and include: Bargut, Chinese individuals from Hong Kong, Han, and Mongolian (Table 5). Table 5 includes the sample size, the references from which the samples were collected, and the label(s) given by the researchers who submitted the sequences to GenBank.

Bargut

The Bargut, or Barga Mongols, are a subdivision of the Mongol people that gave their name to the Baikal region, "Bargujin-Tukum" or the land's end. In the 12th- and 13th-centuries, the Bargut appeared as tribes near Lake Baikal, a lake located in southern Siberia. Today, the Bargut reside in Hulunbuir, a region in northeastern Inner Mongolia in China (Nimaev 2010). Barguts speak the Barga language, which has been spoken since the 17th- and 18th-centuries in the territory of Hulunbuir. Barga is a dialect of the Buryat language (Janhunen 2003).

Chinese Individuals from Hong Kong

This sample was collected by Irwin et al. (2009) and consists of mtDNA control region sequences from 377 residents of urban Hong Kong with Chinese ancestry. Irwin et al. (2009) found the distribution of this data set to be consistent with what has been seen in other Chinese populations. For the purposes of this study, I am using this sample to broadly represent Chinese individuals from a variety of different ethnic backgrounds.

Han

The name Han is derived from a river in central China. It was also the basis for the name of China's Han dynasty, 206 B.C.E.—220 C.E. The Han are the dominant

population in China, Singapore, and Taiwan; they are the population generally referred to as Chinese by those in the West. The Han are distinguishable in regards to both language and culture from the 55 other national minorities in China (West 2009). The foundation of the Han people is distinguishable from about 4000 BCE, when the Yellow River basin was inhabited by farming people with domesticated animals, pottery, and other material culture that indicates they were the antecedents of the Han (Danver 2013; West 2009).

Mongols

The Mongols are a tribal group and live mainly in Mongolia, Inner Mongolia in China, and Russia, in the area where it borders Mongolia. A wider definition of Mongols includes all people that speak Mongolic languages, such as the Buryats and Kalmyks, as well as the Mongols (West 2009). The first reference to the Mongols categorizes them as a Tang dynasty tribe of Shiwei in the 8th-century. It was not until after the fall of the Liao dynasty in 1125 that the Mongols became an important tribe on the Central Asian steppe (Morgan 2007; West 2009).

TABLE 5. *East Asia Sample Composition*

Population/Location	N	Reference	Label/Collection Location
Bargut	7	Derenko et al. (2012)	Bargut
	13	Derenko et al. (2010)	Bargut
Chinese (Hong Kong)	377	Irwin et al. (2009)	ChiHK/urban Hong Kong
Han	1	Macaulay et al. (2005)	Han
	15	Ji et al. (2012)	Han
Mongolia	2	Derenko et al. (2012)	Mongolia
	4	Ingman and Gyllensten (2007)	Mongolian
	1	Pala et al. (2012)	Mongol
	1	Kong et al. (2003)	Mongolian from Inner Mongolia
	1	Olivieri et al. (2013)	Mongolia: Khentii
	422		

East Europe

Twenty populations were sample from this geographic area. The populations sampled include: Albania, Belarus, Bosnia, Bulgaria, Chuvash, Csango, Czech Republic, Estonia, Hungary, Lithuania, Kalmyk, Moldova, Poland, Roma, Romania, Russia, Slovakia, Szekely, Tatars (Volga), and Ukraine (Table 6). Table 6 includes the sample size, the references from which the samples were collected, and the label(s) given by the researchers who submitted the sequences to GenBank.

Albanians

Albania is situated in southeastern Europe and is bordered by Montenegro to the northwest, Kosovo to the northeast, Macedonia to the east, and Greece to the south (Parrish 2017a). The origin of the Albanians can be traced to a population of Illyrian

tribes—Indo-European tribes from the Balkans of southeastern Europe. These tribes had extensive contacts with Romans over seven centuries (Vickers 2014). Beginning in the fifth century, the fusion of mountain tribes and acculturated Illyrians on the coast of the Adriatic Sea eventually resulted in the modern Albanian ethnicity. The main area of Albanian settlement includes parts of Albania and Kosovo, both of which are in the Balkans region (Danver 2013).

Belarusians

Belarus is a landlocked country in Eastern Europe. It is bordered by Russia to the northeast, to the south by Ukraine, to the west by Poland, and to the northwest by Latvia and Lithuania (Means 2017). The Belarusians belong to the eastern group of Slavic peoples, along with Russians and Ukrainians. The name Belarusian is used by this group to distinguish themselves from Russians, and means white Russians (Danver 2013). Most Belarusians are descendants of several East Slav tribes including Dregovichs, Krivichs, and Radimichs, as well as the Yotvingians, a Baltic tribe who lived in the northwest of modern Belarus (Savchenko 2009).

Bosniaks

Bosniaks are Bosnian Muslims living primarily in Bosnia and Herzegovina, in southeastern Europe on the Balkan Peninsula (Danver 2013). They make up roughly half of the Bosnian population, which also includes Serbs and Croats. The ancestors of the Bosniaks were Slavic migrants who arrived in the Balkans in the 7th-century and settled in modern-day Bosnia and Herzegovina (Danver 2013; Davies 1996).

Bulgarians

Bulgaria is on the Balkan Peninsula in southeastern Europe. It is bounded by Romania to the north, Turkey and Greece to the South, Macedonia to the southwest, Montenegro and Serbia to the west, and the Black Sea to the east (Parrish 2017b). The ancestry and name of the Bulgarians can be traced to the Bulgar. The Bulgar were a Turkic people that ruled over Slavic populations in the area south of the Danube River during the Middle Ages. A distinctive Bulgarian ethnicity arose from the cultural fusion of the Bulgars with ancient Thracian tribes and the Slavic peoples of the region (Crampton 2005; Danver 2013).

Chuvash

The Chuvash mainly live in the Republic of Chuvashia, located on the banks of the Volga River in the center of European Russia. They are a Turkic people whose name can be traced to the tribes of Volga Bulgaria—called *suvar* or *suvaz* (Danver 2013). A unique Chuvash ethnicity developed in the 7th- and 8th-centuries when Turkic tribes settled around the Middle Volga River. These tribes were mostly of Bulgarian origin and mixed with the local Finno-Ugric population. In the 15th- and 16th-centuries, the Chuvash were ruled by the Kazan khanate, officially becoming Russian subjects in 1551 (Danver 2013; Róna-Tas 1982).

Csango

The Csango live in present-day Romania. Some research suggests that the Csango are some of the first Hungarian settlers in Romania (Brandstätter et al. 2007). The ethnic background of the Csango is disputed. One view postulates that the Csango

people descended from a group left behind by the Magyars in 896 BCE. This has been reinforced by genetic analyses (Guglielmino and Beres 1996). Today, the Csango are made up of several heterogeneous groups divided by origin and location. The Csango are distinct from other Hungarian ethnic groups because of their language, traditions, and folklore (Brandstätter et al. 2007). Most likely both the Csango and Szekely (discussed below) are related to the Magyars (Guglielmino and Beres 1996), and diverge in more recent historical background (Brandstätter et al. 2007).

Czechs

The Czech Republic is a landlocked state located in Central Europe. It is bordered to the south by Austria, Germany to the west, Poland to the northeast, and Slovakia to the east (Roux 2004). It includes the historic territories of Bohemia and Moravia. Czechs are descended from the medieval Slavic peoples of Bohemia and Moravia (Cravens 2006; Danver 2013).

Estonians

Estonians, a Finnic people, primarily reside in Estonia, located in the Baltic region of Northern Europe bordering the Baltic Sea to the west (Danver 2013). Although Estonia is grouped as a Baltic country, along with Latvia and Lithuania; Estonians are ethnically and linguistically unrelated to the other Baltic peoples. Rather, they are most closely connected to the Finns (Bertriko 2004; Danver 2013).

Hungarians

Hungary is located in Central Europe and is bordered by Austria and Slovenia to the west, Romania and Ukraine to the east, Slovakia to the north, and Croatia and Serbia

to the south (Nagy 2017). Hungarians reside primarily in Hungary, and are a Finno-Ugric people related to Estonians and Finns. The Hungarians are affiliated most directly with two Ugric populations, the Mansi (Voguls) and the Khanty (Ostyaks) (Sugar et al. 1990). The Hungarians are the only Finno-Ugric population to migrate as far as Central Europe; in fact, they migrated westward while other Ugric peoples moved into Siberia (Danver 2013; Sugar et al. 1990).

Kalmyks

Kalmyks are a Mongolian people living in southwestern Russia. They trace their ancestry to the Oirats, a Western Mongolian tribe that migrated from Central Asia to Europe in the 17th-century (Danver 2013). The Kalmyks appeared as a unique ethnic group in the periphery of Europe along the western coast of the Caspian Sea. Today, the Kalmyks inhabit the Republic of Kalmykia (Chal'mg-Tanhch in Kalmykian), which is a subject of the Russian Federation (Danver 2013; Guchinova 2006).

Lithuanians

Lithuanians are a Baltic people mostly residing in Lithuania, the largest and southernmost of the Baltic states in Eastern Europe. Lithuanian ethnicity arose from an assortment of eastern Baltic tribes, including the Curonians, Prussians, Samogitians, and Selonians (Danver 2013). The ancestors of the Lithuanians initially settled in the area spanning the Daugava and Vistula Rivers, but Slavic migrations led to overpopulation of formerly Baltic lands and, as a result, the shrinking of Baltic settlement after 700 C.E. (Danver 2013; Kiaupa 2002).

Moldovans

The Republic of Moldova is located in the northeastern corner of Eastern Europe, between Ukraine and Romania (Danver 2013). Moldovans are the most populous ethnic group in this country. Moldovans share both linguistic and cultural traits with Romanians, and there is some debate about whether Moldovans are a separate ethnic group or simply a subset of Romanians (Danver 2013; King 2000).

Polish

Poland is a country in Central Europe bordered by Belarus, Czech Republic, Germany, Lithuania, Slovakia, and Ukraine (Grajnert 2002). The Poles are the native people of Poland, and are the result of the blending of a number of West Slavic populations between the 6th- and 9th-centuries. However, a distinctive Polish ethnic identity did not emerge until the 11th-century. Prior to this, the population of modern-day Poland was called Slavic, and the country was referred to as Sclavinia, or "land of the Slavs" (Danver 2013; Lukowski and Zawadzki 2006).

Roma

The Roma are a traditionally itinerant people that trace their origin to northern India, but now live mostly in Europe (Alfonso Sánchez et al. 2018; Danver 2013). Although they are dispersed across more than 35 countries within Europe, the sample that I have included is from Hungary. Roma were first documented in Europe in the 12th-century. Despite having originated in India, the ethnic identity of the Roma developed in Europe (Fraser 1992). Throughout much of their history, the Roma have lived

segregated from the majority population. Even today, in the Balkan region, that is still the case (Fekete 2014).

Romanians

Romanians are the native people of Romania, an Eastern European country bordered by Bulgaria, Hungary, Moldova, Serbia, and Ukraine, as well as the Black Sea to the southeast (Aronson 2017). The name Romanian is a reflection of their origins during the time when the Roman Empire reigned over the region. Modern Romanians are the descendants of the Dacians, an Indo-European group that inhabited the Balkan Peninsula prior to Roman invasion (Danver 2013; Hitchins 2014).

Russians

Russia, or the Russian Federation, is the largest country in the world and is located in Eurasia. It spans the entirety of Northern Asia and most of Eastern Europe (Tucci and Rosenberg 2009). Russians are the most populous ethnic group in Russia; in fact, in all of Europe. Russian ethnicity emerged approximately 1,000 years ago when a group of eastern Slavic tribes was united under the rule of Kiev, or "mother of Russian cities," on the Middle Dnieper River (Danver 2013; Gilbert 2007).

Slovaks

The Slovaks are a Slavic people that live mostly in Slovakia and the surrounding countries in Central Europe. Slovakia, or the Slovak Republic, is a country in Central Europe, bounded by Austria, the Czech Republic, Hungary, Poland, and Ukraine (Kirschbaum 2005). Modern-day Slovakia was settled in the 5th- and 6th-centuries by Slavic populations. The Avars, a nomadic people that migrated from the Eurasian steppe,

were the first to exert control over the region, but Avar rule ended in 822 and local rulers in the lands of the western Slavs took over (Danver 2013; Kirschbaum 2005).

Szekely

The Szekely are one of the largest Hungarian populations in Transylvania. They live primarily in the Harghita and Kovaszna counties of Romania (Brandstätter et al. 2007). The origins of the Szekely are much debated. Different theories suggest that the Szekely have "Eurasian Avar (a Turkic-speaking tribe who migrated from eastern Asia into central and eastern Europe in the 6th-century), Gepid (a Germanic tribe), Bulgar-Turk (warrior people from the delta of the Volga River), or Hunnish (Central Asian nomads) ancestry" (Brandstätter et al. 2007:792). Some research has suggested that the Szekely have been in the eastern Carpathians since the 5th-century, while others have suggested that they are a Hungarian group that settled in Transylvania to protect the country's borders (Goedde et al. 1991). Yet other theories suggest that the Szekely are descended from the Magyars and the cultural differences are due to geographic isolation (De Silvestri 2000). In spite of the overabundance of theories, the only undisputed fact is that the Szekely have occupied the same area of Transylvania since the beginning of the 13th-century (Brandstätter et al. 2007).

Volga Tatars

Volga Tatars reside mostly in western Russia along the Volga River, and are a Turkic-speaking people. The name Tatar likely came from Mongolian Tatars in the 5th-century, but has only been in use since the end of the 19th-century as an ethnic category (Danver 2013). The Kipchak peoples and the Volga Bulgars, the Turkic ancestors of the

Tatars, migrated from Central Asia to Eastern Europe in the 7th-century; thus, the emergence of a unique Tatar ethnicity took place in Europe (Yémelianova 1997).

Ukrainians

Ukraine spans the Black Sea between Russia and the rest of Eastern Europe. Ukrainians are the major ethnic group in Ukraine and are descendants of Slavic populations that migrated to the area around the first millennium C.E. (Reid 1999). Belarussians, Russians, and Ukrainians are all Slavic peoples and have been neighbors since the Middle Ages. The ethnic differentiation of these groups was a lengthy process that took place from the 12th- to the 14th-century (Danver 2013; Reid 1999).

TABLE 6. *East Europe Sample Composition*

Population/Location	N	Reference	Label/Collection Location
Albania	2	Pala et al. (2012)	Albania
	1	Kushniarevich et al. (2013)	Albania
	1	Gasparre et al. (2007)	Albania
	1	Behar et al. (2012)	Albania83
Belarus	3	Pala et al. (2012)	Belarus
	4	Malyarchuk et al. (2008a)	Belarus
	13	Malyarchuk et al. (2010b)	Belarus
Bosnia	1	Pala et al. (2012)	Bosnia and Herzegovina
	1	De Fanti et al. (2015)	Bosnia and Herzegovina
	1	Direct submission	Bosnia and Herzegovina
	1	Pala et al. (2009)	Bosnia and Herzegovina
	1	Kovacevic et al. (2014)	Bos20
Bulgaria	3	Fernandes et al. (2012)	Bulgaria
	1	Gandini et al. (Unpublished)	Bulgaria
	16	Direct submission	Bulgaria
Chuvash	3	Derenko et al. (2012)	Chuvash
	1	Fernandes et al. (2012)	Chuvash
Csango	100	(Brandstätter et al. 2007)	Csango

TABLE 6. *continued*

Population/Location	N	Reference	Label/Collection Location
Czech Republic	1	Pala et al. (2012)	Czech Republic
	8	Mielnik-Sikorska et al. (2013)	CZ
	1	Malyarchuk et al. (2008b)	Czech Republic
	1	Derenko et al. (2012)	Czech
	1	Derenko et al. (2010)	Czech
	8	Malyarchuk et al. (2008a)	Czech Republic
Estonia	5	Pala et al. (2012)	Estonia
	1	Direct submission	Estonian
	1	Pala et al. (2009)	Estonia
Hungary	211	Irwin et al. (2007)	Budapest
Kalmyk	3	Derenko et al. (2012)	Kalmyk
	2	Derenko et al. (2010)	Kalmyk
	1	Palanichamy et al. (2015)	Kalmyk
Lithuania	3	Pala et al. (2012)	Lithuania
	9	Direct submission	Lithuania
Moldova	1	Pala et al. (2012)	Moldova
	1	De Fanti et al. (2015)	Moldova: Gagauzis
	2	Direct submission	Moldova
Poland	1	Pala et al. (2012)	Poland
	19	Mielnik-Sikorska et al. (2013)	Polish
Roma	205	Irwin et al. (2007)	Roma
Romania	10	Pala et al. (2012)	Romania
	2	Kushniarevich et al. (2013)	Romania
	5	Gandini et al. (Unpublished)	Romania
Russia	151	Irwin et al. (2010)	Individual with ancestry from western Russia
Slovakia	1	Pala et al. (2012)	Slovakia
	11	Mielnik-Sikorska et al. (2013)	Slovakia
	2	Malyarchuk et al. (2008b)	Slovakia
	6	Malyarchuk et al. (2008a)	Slovakia
Szekely	178	Brandstätter et al. (2007)	Szekely
Tatars	1	Derenko et al. (2012)	Tatar

TABLE 6. *continued*

Population/Location	N	Reference	Label/Collection Location
Tatars (con't)	19	Malyarchuk et al. (2010a)	Russia
Ukraine	10	Pala et al. (2012)	Ukraine
	7	Mielnik-Sikorska et al. (2013)	UKR
	3	Olivieri et al. (2013)	Ukraine
	1045		

Near East

Thirteen populations were sampled from this geographic area. The populations sampled include: Cyprus, Dubai (UAE), Iran, Iraq, Israel, Jordan, Kuwait, Lebanon, Palestine, Saudi Arabia, Syria, Turkey and Yemen (Table 7). Table 7 includes the sample size, the references from which the samples were collected, and the label(s) given by the researchers who submitted the sequences to GenBank.

Cypriots

The Cypriots reside on the island of Cyprus, located in the eastern Mediterranean Sea, and are a Greek people. They are descendants of Greek settlers who migrated there in the 12th- and 11th-centuries B.C.E. (Danver 2013). The Cypriots have a long history of being directly and indirectly ruled by foreign powers, but it was not until the Turkish occupation that the proportions of the population on Cyprus changed. During the period of Ottoman colonial rule, Turkish migrants moved to the island and settled in the north. Today, Cyprus is divided along ethnic lines; although, the secession of the Turkish portion of Cyprus is not internationally recognized (Danver 2013; Ker-Lindsay 2011).

Dubai (Emiratis)

Seven emirates make up the United Arab Emirates, and Dubai is the second largest. Dubai's population is made up primarily of expatriates from South and Southeast Asia, with a quarter of the expatriate population tracing their origins to neighboring Iran. UAE nationals (Emiratis) constitute a minority. The Dubai sample is made up of male citizens of Dubai identified as Dubai Nationals based on physical appearance and language (Alshamali et al. 2008).

Iranians

Historically, Iran was known as the Persian Empire. The name Iran derives from Iryana, meaning "land of Aryans" (Danver 2013). Iran is an ethnically diverse nation that is located in southwestern Asia, and borders Afghanistan, Azerbaijan, Iraq, and Pakistan. Ancient Iran was home to a number of tribes that shared cultural traits and all spoke a common Proto-Iranian language. In the 7th-century BCE, these tribes were unified by the Medes and expanded the borders of Iran into Central Asia (Curzon 2001). Today, a little over half of all Iranians have Persian descent (Danver 2013).

Iraqis

Iraq occupies an area that corresponds to the ancient civilization of Mesopotamia, located between the Euphrates and Tigris Rivers. It is located in southwestern Asia, bordering Turkey, Iran, Kuwait, Saudi Arabia, Jordan, Syria, and the Persian Gulf (Danver 2013). Mesopotamia was ruled by a series of local populations, including the Akkadians, Amorites, Assyrians, and Chaldeans, until it was conquered by foreign powers in the 7th-century. Because of the Arabization carried out by the Muslim

caliphates, like the Ottoman, that ruled Iraq from the 7th-century until the 19th-century, Iraq's indigenous people have had to hide their identities. Despite this, many Iraqi native groups have survived and Iraqi society today encompasses a wide variety of ethnic groups and religious sects (Curzon 2001; Danver 2013). Today, Arabs constitute roughly 75% of the population of Iraq (Danver 2013).

Israelis

Israel is located on the eastern shore of the Mediterranean Sea. It borders Egypt and the Gaza Strip, Jordan and the West Bank, Lebanon, and Syria (Danver 2013). The history of Israel and its native occupants is a matter of much debate, but the beginning of Israeli nationhood seems to date back to 1800 BCE. This is the year that Israelites came to Canaan, a region that corresponds with modern-day Israeli and Palestinian territories (Noll 2001). The Israelites were a Semitic-speaking people, considered to be an outgrowth of the indigenous populations that had long inhabited ancient Israel, the Southern Levant, Syria, and Transjordan (Finkelstein 1996). In 1200 BCE, Canaan was again occupied by Israelite tribes upon their return from Egypt. Over the next nine centuries, various conquerors, including the Greeks, Persians, and Romans, overwhelmed the area. Despite this instability, scholars argue that the Israelites never quite disappeared from the area until the 12th-century Christian Crusades, during which they were nearly eradicated as a people (Danver 2013; Noll 2001). In 1917, the British government pledged to support a proposal to help Jewish people return to Jerusalem and over the next three decades the Jewish community in Palestine expanded from 85,000 to 650,000. Today, the majority of people in Israel are of Jewish descent (Danver 2013).

Jordanians

Jordan is located in southwest Asia, bordering Syria, Iraq, Saudi Arabia, Israel, and the West Bank. It was once part of the Ottoman Empire and later, during British rule, was known as Transjordan. Jordan was the site of some of the earliest human settlements with archaeological sites dating to the early Paleolithic. Jordan's population is 98% Arab and can be divided into three main groups: the Bedouin, Palestinian Arabs, and Transjordanians. The Bedouin are often considered the indigenous people of Jordan and make up a large portion of the country's population. Transjordanians are the Arab group that live east of the Jordan River and were settled in the area prior to 1948. Palestinian Arabs either moved to Jordan from the West Bank or are refugees of the Arab-Israeli wars and the Persian Gulf War (Skinner 2003; Thornberry and Bruce-Mitford 1990).

Kuwaitis

Kuwait is in the heart of the Middle East. It shares a land border with Iraq and another with Saudi Arabia. The majority of Kuwaiti citizens are ethnically Arab, which means they can trace their ancestry to the Arabian Peninsula before the advent of Islam. It is not clear exactly how long Kuwait has been occupied, but it is evident that it was home to a series of different people. Migrants came to the area to conduct trade or searching for opportunities for prosperity in the pearling industry, while others came because they were driven from their homes by harsh weather (Alenizi et al. 2008; Alsmadi et al. 2013; Casey 2007).

Lebanese

Lebanon is located in western Asia and is bordered by Israel, Syria, and the Mediterranean Sea. It has a rich history filled with religious and ethnic diversity (Harris 2012). The Levant has been occupied by human populations for a very long time, and about 3 to 4 thousand years ago a Semitic-speaking people called the Canaanites emerged in the region as a distinctive culture. The Canaanites, who were known to the ancient Greeks as the Phoenicians, colonized territories throughout the Mediterranean and even got so far as the Iberian Peninsula (Markoe 2000). There are questions surrounding the origins of the Canaanites, but modern researchers have found archaeological and historical evidence of population continuity for millennia in this region. The modern-day Lebanese people get most of their ancestry from a Canaanite-related population. They also have some Eurasian ancestry, which seems to be the result of more recent admixture (Haber et al. 2017).

Palestinians

It is not clear where the term Palestinian originated. Some historians associate it with the Philistines, a biblical people from the eastern coast of the Mediterranean Sea. As such, some consider Palestinians to be the indigenous people of present-day Israel, the West Bank, and the Gaza Strip (Danver 2013). As previously mentioned, this viewpoint is disputed by scholars who assert that Jews and others resided in Palestine prior to Arab arrival in the 7th-century (Pappé 2006). In light of this disputed history, the emergence of Palestinians as a cohesive group was the result of their encounter with the Jewish nationalist movement. As European Jews implemented a plan to reconstitute a

Jewish homeland in Palestine, the Arab peoples living there were put into a unique and ultimately devastating situation (Danver 2013; Pappé 2006).

Saudi Arabians

Saudi Arabia is named for ‘Abd al-‘Aziz al-Sa’ud, who led his warriors to found a modern state in the 20th-century. Arabia derives from Arab, which referred to the Arabic-speaking tribes that had a nomadic lifestyle (Zuhur 2012). Saudi Arabia is located in southwestern Asia on the Arabian Peninsula. It borders Oman, Yemen, and the United Arab Emirates, as well as Iraq, Jordan, and Kuwait. It has water borders with both the Red Sea and the Persian Gulf (Belanger 2017). Numerous migrations from Asia and Africa have taken place here since ancient times and, because of its strategic location, Saudi Arabia was a critical area for cultural exchange, trade, and warfare (Abu-Amero et al. 2007). The rise of Islam in the 7th-century CE changed the Arabian Peninsula dramatically and within a short span of time Arabs had built an empire that stretched from Pakistan to the Iberian Peninsula (Abu-Amero et al. 2008). Today, the vast majority of the population of Saudi Arabia is Arabs with other ethnic groups making up roughly 10% (Zuhur 2012).

Syrians

Syria is located on the eastern coast of the Mediterranean Sea, bordering Iraq, Israel, Jordan, Lebanon, and Turkey (Danver 2013). It is a predominantly Arab nation with a long history of occupation by various Semitic tribes including Canaanites and Arameans. The region was conquered by the Macedonians in the 4th-century BCE and

defeated by the Romans in the 2nd- and 3rd-centuries BCE (Nisan 2002). All of these conquests resulted in a region that is a hybrid of many different cultures (Danver 2013).

Turks

Turkey is located between Asia and Europe and stretches across Asia Minor. The population is primarily made up of people of Turkish descent (Danver 2013). Anatolia, 97% of the territory of Turkey, is one of the longest inhabited areas of the world. In the 9th-century, Turkmen raids resulted in Turkish settlement of the region; and, in 1075, Turkmen established the Anatolian Seljuk state. This lasted until the Mongol invasion in 1243, which was followed by a wave of Turkmen tribes settling in the area and the final Turkification of the region (Danver 2013; Zürcher 2004).

Yemenis

Yemen occupies the southwestern corner of the Arabian Peninsula and is bordered to the west by the Red Sea. The Yemeni population is mainly Arab; although, a small percentage of the population has African and Asian ancestry. Prior to the introduction of Islam in the 6th-century CE, the South Arabian kingdoms declined and the conquests of Ethiopian and Persian rulers failed. In the 9th-century, leadership under the Zaydi imams began. Between the 11th- and 14th-centuries, various dynasties, both local and external, struggled for power in the region. In the early 1900s, the imams reasserted their political authority over the tribes of Yemen and against Saudi Arabia (Khanam 2005).

TABLE 7. *Near East Sample Composition*

Population/Location	N	Reference	Label/Collection Location
Cyprus	91	Irwin et al. (2008)	Cyprus
Dubai (UAE)	3	Pala et al. (2012)	United Arab Emirates: Dubai
	8	Fernandes et al. (2012)	United Arab Emirates: Dubai
	1	Gandini et al. (Unpublished)	United Arab Emirates: Dubai
Iran	18	Pala et al. (2012)	Iran
	2	Schonberg et al. (2011)	Iranian
Iraq	182	Al-Zahery et al. (2013)	Arab Muslims Living in Baghdad
Israel	7	Pala et al. (2012)	Israel
	4	Behar et al. (2006)	Israel
	1	Olivieri et al. (2006)	Israel
	1	Achilli et al. (2004)	Israel
	3	Fernandes et al. (2012)	Israel
Jordan	1	Pala et al. (2012)	Jordan
	1	Roostalu et al. (2007)	Jordanian #923
	6	Maca-Meyer et al. (2001)	Jordan
	1	García et al. (2011)	Jordan
	1	Ennafaa et al. (2009)	Jordan
	2	González et al. (2007)	Jordan
Kuwait	381	Scheible et al. (2011)	Kuwait
	2	Olivieri et al. (2013)	Kuwait
	1	Kushniarevich et al. (2013)	Kuwait
	2	Pennarun et al. (2012)	Kuwait
Lebanon	1	Pala et al. (2012)	Lebanon
	1	Behar et al. (2006)	Lebanon
	1	Kushniarevich et al. (2013)	Lebanon
	2	Gandini et al. (unpub)	Lebanon
	15	Matisoo-Smith et al. (2016)	Lebanon
Palestine	1	Pala et al. (2012)	Palestinian
	1	Behar et al. (2006)	Palestine
	5	Gandini et al. (Unpublished)	Palestine, Gaza
	2	Pereira et al. (2010)	Palestinian
Saudi Arabia	1	Pala et al. (2012)	Saudi Arabia

TABLE 7. *continued*

Population/Location	N	Reference	Label/Collection Location
Saudi Arabia (con't)	1	Behar et al. (2006)	Saudi Arabia
	2	Kushniarevich et al. (2013)	Saudi Arabia
	2	Pennarun et al. (2012)	Saudi Arabia
	7	Abu-Amero et al. (2007)	Saudi Arabia
	5	Abu-Amero et al. (2008)	Saudi Arabia
Syria	3	Pala et al. (2012)	Syria
	1	Behar et al. (2006)	Syria
	1	Gandini et al. (Unpublished)	Syria
	1	Behar et al. (2012)	Syria
Turkey	9	Pala et al. (2012)	Turkey
	11	Schonberg et al. (2011)	Turk
Yemen	3	Pala et al. (2012)	Yemen
	2	Achilli et al. (2005)	Yemen
	3	Behar et al. (2006)	Yemen
	11	Fernandes et al. (2012)	Yemen
	806		

North Asia

Four populations were sampled and include: Evenki, Mansi, Nganasan, and Yakut (Table 8). Table 8 includes the sample size, the references from which the samples were collected, and the label(s) given by the researchers who submitted the sequences to GenBank.

Evenki

The Evenki are one of the most numerous and widely scattered indigenous peoples of northern Siberia. They also live in Mongolia and China, where they are one of 55 recognized minority groups (Levin and Potapov 1964; West 2009). In the past,

Evenki were called Tungus and were grouped together with several other related groups, including the Even and Negidal. The region around Lake Baikal in southern Siberia was the original home of all Tungusic people. The Evenki migrated eastward from there, toward the Amur River, and northward as far as the Arctic Ocean. This migration most likely occurred at the beginning of the first millennium when pressure from Turkic peoples forced other groups to either assimilate or move (West 2009). The Evenki language is from the northern branch of the Tunguso-Manchurian language group, and is closely related to both the Even and Negidal languages (Levin and Potapov 1964; MacKenzie 2005).

Mansi

The Mansi, obsoletely known as the Voguls, live in Khanty-Mansia, an autonomous district within Tyumen Oblast in the western Siberian region of Russia. The Mansi language, along with Hungarian and Khanty, forms the Ugrian group of the Uralic languages. The origins of the Mansi trace back to the area west of the Urals, where their ancestors resided. In the first millennium, they migrated to western Siberia and assimilated the local inhabitants (Kolga et al. 2001; Levin and Potapov 1964).

Nganasan

The Nganasans inhabit the Taymyr Peninsula in north Siberia, and are the most northerly people of Russia (Levin and Potapov 1964). The Nganasan language belongs to the Samoyedic branch of the Uralic language family (Janhunen 1998). The Ngansans are considered to have arisen as an ethnic group when Samoyedic people migrated from the south to the Taymyr Peninsula encountering Paleo-Siberian peoples along the way.

They were traditionally a semi-nomadic reindeer hunting group until they were settled in the villages where they live now in the 1970s (Popov 1966).

Yakut

The Yakuts live in the republic of Sakha (formerly called Yakutia), which is part of the Far Eastern Federal District of Russia. The Yakut are also known by their ethnic name, Sakha (Danver 2013). They originated in the Lake Baikal region, but were forced north as the result of Mongol invasions during the 13th century. Until the 17th century, Yakuts were the main colonizers of eastern Siberia. Smaller Siberian groups like the Tungus were assimilated into Yakut culture (Danver 2013; Levin and Potapov 1964). The Yakut language is a part of the Siberian branch of Turkic languages (Levin and Potapov 1964).

TABLE 8. *North Asia Sample Composition*

Population/Location	N	Reference	Label/Collection Location
Evenki	10	Derenko et al. (2010)	Evenk
	1	Derenko et al. (2007)	Evenk
	1	Ingman et al. (2000)	From Evenki individual
	1	Starikovskaya et al. (2005)	EvenkiC2a
	1	Mishmar et al. (2003)	Evenki
	1	Sukernik et al. (2012)	Evenki
	4	Volodko et al. (2008)	Evenk individual
Mansi	4	Ingman and Gyllensten (2007)	Mansi
	2	Starikovskaya et al. (2005)	Mansi
	6	Sukernik et al. (2012)	Mansi
Nganasan	3	Starikovskaya et al. (2005)	Nganasan
	2	Sukernik et al. (2012)	Nganasan
	6	Volodko et al. (2008)	Avam Nganasan
	1	Derbeneva et al. (2002b)	Nganasan Avam
Yakut	1	Achilli et al. (2005)	Yakut
	1	Derenko et al. (2012)	Yakut
	3	Derenko et al. (2010)	Yakut
	1	Derenko et al. (2007)	Yakut
	4	Ingman and Gyllensten (2007)	Yakut
	1	Derenko et al. (2014)	Yakut
	54		

North/Central Asia

Eleven populations were sampled from this region including: Altaian Kazakh, Altaian Kizhi, Buryat, Ket, Khamnigan, Shor, Teleut, Tofalar, Tubular, Tuvinian, and Uyghur (Table 9). Table 9 includes the sample size, the references from which the samples were collected, and the label(s) given by the researchers who submitted the sequences to GenBank.

Altaian Kazakhs

The predecessors of the Altaian Kazakhs emerged as a distinctive group when members of the Kerei tribe of the Kazakh Middle Horde moved into northwestern China and western Mongolia in the 18th century (Gokcumen et al. 2008; Golden 1992). Subsequently, they set up a nomadic lifestyle in the Altai-Sayan region, Xinjiang, and Western Mongolia (Gladney 1996). Further Russian migrations into traditionally held Kazakh lands may have forced other Kazakh groups to follow this example. In the 19th century, groups of Chinese and Mongolian Kazakhs moved into the northern slopes of the Altai-Sayan Mountains (Gladney 2003). Today, Altaian Kazakhs live in remote mountainous parts of the Altai Republic, Mongolia, and northern China (Dulik et al. 2011; Gokcumen et al. 2008).

Altaian Kizhi

In general, the Altai are a group of Turkic peoples who reside in southern Siberia in the area bordering western Mongolia to the south. They are typically divided into two groups, the Northern and the Southern Altai. The Southern Altai are often referred to as the Altaian Kizhi, meaning Altaian man or person. The Altaian Kizhi have been significantly influenced by Mongolians and resemble them physically (West 2009). Today, the Altai primarily live in the Altai Republic of the Russian Federation, located along the border with Mongolia (Danver 2013). The area surrounding the Altai Mountains is considered the birthplace of the Turkic people, and it is widely believed that the ancestors of the Altai have been living in this area for thousands of years (West 2009).

Buryats

The Buryats primarily reside in the Republic of Buryatia in Siberia, Russia (West 2009). They are Mongol by descent and their pre-Russian history is essentially the history of the Mongolian people more generally (Boldonova 2016). The Buryats trace their ancestry to Genghis Khan's mother, who was born on the eastern shore of Lake Baikal. They see this as an important source of their historical identity (West 2009).

Ket

The Ket of Central Siberia (also known as Yenisei Ostyak) are linguistically related to Athabascan-speaking tribes of Native Americans. The Ket live mainly in isolated villages on the Yenisei River in Russia's Krasnoyarsk Territory, located in the middle of Siberia. They were the last hunter-gatherer group in landlocked northern Eurasia and only settled down in the 1930s (Danver 2013).

Khamnigan

The Khamnigan, or the Horse Tungus, come from Transbaikalia, a mountainous region east of Lake Baikal in Russia. The native territory of the Khamnigan is made up of the Argun and Onon basins in northeastern Mongolia and northwestern Manchuria. In Mongol history, the Khamnigan occupy a very important region because this is where Genghis Khan was born and where he began the consolidation of the Mongol tribes. The Russians traditionally identified the Khamnigan as Tungus, while modern China classifies them as Evenki. This difference in identifications is due to the fact that as an ethnic group the Khamnigan are a composite of Mongolic and Tungusic groups. The dual affiliation of the Khamnigan is easy to trace in their social background as well as

their bilingualism. They have two native languages, one Mongolic and the other Tungusic. The Tungusic language is what their neighbors have historically used to classify them. In fact, the term Khamnigan is the Mongolic name for the Evenki (Janhunen 2003).

Shor

The Shors are a Turkic-speaking people residing in the Tom basin along the Kondoma and Mras-Su Rivers in Kemerovo Oblast, Russia. They also live in the Republic of Khakassia and the Altai Republic, both federal subjects of Russia (Forsyth 1992; Levin and Potapov 1964). The modern-day Shors are the Turkicized descendants of the Ugrian Samoyedic-speaking tribes and Yeniseian-speaking indigenous peoples of the northern taiga region of the Altai and Sayan Mountains (Levin and Potapov 1964).

Teleut

The Teleuts are a Turkic-people residing in the south of western Siberian, primarily in rural areas and towns in Kemerovo Oblast, Altai Krai, and the Altai Republic (Forsyth 1992; Swarovskaya et al. 2015). They speak one of the southern dialects of the Altai language. The Teleuts are descendants of the tribes of ancient Turks. Russian chroniclers first referred to the Teleuts or white Kalmyks (as opposed to black Kalmyks, i.e., Mongolians) at the beginning of the 17th century. The Teleuts participated in the ethnogenesis of many neighboring peoples including Altaians, Khakassians, Tatars, and Russians, and assimilated over time with these groups (Swarovskaya et al. 2015).

Tofalar

The Tofalar (or Karagasys) are a small tribe of Turkic-origin living in the northern slopes of the Sayan Mountains, located in southern Siberia, Russia (Starikovskaya et al. 2005). Originally, the Tofalar spoke a Samoyed language, which comes from the Uralic language family, but they later took on a Turkic language (Levin and Potapov 1964; Starikovskaya et al. 2005). The Tofalar are close to the eastern Tuvans-Todzhins in terms of language and culture (Levin and Potapov 1964).

Tubular

The Tubular are recent descendants of small hunter-gatherer groups who lived in the coniferous forest area of northeastern Altai. They are different from Southern Altaians (Altaian Kizhi) in culture, language, and appearance (Levin and Potapov 1964; Starikovskaya et al. 2005). The Tubular are closely related to the Tofalar; and, in fact, the Tofalar call themselves Tubular (Levin and Potapov 1964).

Tuvinians

The Tuvinians or Tuvans are largely Turkic-speakers who reside in the Tuva Republic, located in the southern extreme of Siberia (Starikovskaya et al. 2005). The Tuvans have a diverse ethnic composition and originate from Turkic-speaking, and to some extent Mongolic-speaking, Samoyedic-speaking, and Yeniseian-speaking ethnic elements. They include some Turkic-speaking groups, known from the Chinese chronicles of the first few centuries CE and from Orkhon inscriptions on stones dating from the 7^{th} and 8^{th} centuries (Levin and Potapov 1964).

Uyghur

The Uyghur primarily live in the Xinjiang Uyghur Autonomous Region of China, and are an official minority nationality of China. Many Uyghur argue that they are the autochthonous people of this region and conceive of their ancestors as having originated in Xinjiang (Gladney 2000). However, historical records show that the Uyghur were an ancient confederation of Turkic tribes that united and established a khanate south of Lake Baikal (Mongolia) in 740 CE. In 840 CE, the Uyghur Kingdom was conquered by the Kyrgyz, another Turkic group, and in the successive years, the original population dispersed to the south and west. Many Uyghur migrated to the southwest and settled in the desert-oasis regions north of the Tarim Basin in modern-day Xinjiang (Khanam 2005).

TABLE 9. *North/Central Asia Sample Composition*

Population/Location	N	Reference	Label/Collection Location
Altaian Kazakh	1	Derenko et al. (2010)	Altaian Kazakh
	1	Derenko et al. (2012)	Altaian Kazakh
	11	Derenko et al. (2014)	Altaian Kazakh
Altaian Kizhi	6	Derenko et al. (2012)	Altaian-Kizhi
	13	Derenko et al. (2010)	Altaian-Kizhi
	1	Derenko et al. (2007)	Altaian-Kizhi
Buryat	12	Derenko et al. (2012)	Buryat
	8	Derenko et al. (2010)	Buryat
Ket	1	Starikovskaya et al. (2005)	Ket33A1
	1	Sukernik et al. (2012)	Ket
	1	Volodko et al. (2008)	Ket individual
	1	Derbeneva et al. (2002a)	Ket2000
Khamnigan	8	Derenko et al. (2012)	Khamnigan
	12	Derenko et al. (2010)	Khamnigan
Shor	2	Derenko et al. (2012)	Shor
	4	Derenko et al. (2010)	Shor
	3	Ingman and Gyllensten (2007)	Shortci
	3	Derenko et al. (2014)	Shorian
Teleut	1	Derenko et al. (2012)	Teleut
	4	Derenko et al. (2010)	Teleut
	1	Derenko et al. (2007)	Teleut
	2	Derenko et al. (2014)	Teleut
Tofalar	3	Starikovskaya et al. (2005)	Tofalar
	1	Mishmar et al. (2003)	Tofalar
Tubular	1	Starikovskaya et al. (2005)	Tubular
	16	Sukernik et al. (2012)	Tubalar
	3	Volodko et al. (2008)	Tubalar individual
Tuvinian	1	Derenko et al. (2012)	Tuvinian
	4	Ingman and Gyllensten (2007)	Tuvinian
	2	Starikovskaya et al. (2005)	Tuvan
	7	Sukernik et al. (2012)	Tuva Republic
	1	Volodko et al. (2008)	Tuvan individual
	2	Derenko et al. (2014)	Tuvinian
Uyghur	1	Zhao et al. (2009)	Uyg5
	1	Direct submission	Uigur population
	140		

North/East Asia

There were eight populations sampled, which include: Chukchi, Even, Koryak, Negidal, Nivkhi, Udegey, Ulchi, and Yukaghir (Table 10). Table 10 includes the sample size, the references from which the samples were collected, and the label(s) given by the researchers who submitted the sequences to GenBank.

Chukchi

The Chukchi people inhabit the Chukchi Peninsula and the shores of the Bering Sea and Chukchi Sea regions of the Arctic Ocean. Although the Chukchi Peninsula has been inhabited for roughly 7,000 years, it appears that the Chukchi were not indigenous to this particular region (West 2009). Instead, the Chukchi likely originated from people living around the Okhotsk Sea and later invaded the Peninsula at an as of yet undetermined date (Forsyth 1992). The Chukchi assimilated many of the indigenous inhabitants and expanded their territory at the expense of others, most markedly the Yupiks (West 2009). The Chukchi share a close kinship with the Koryaks and Itelmens, which is manifested most apparently in their language, but also in aspects of their material and spiritual culture (Levin and Potapov 1964).

Evens

The Evens are an indigenous group of Siberia and the Far East of Russia. They are related to the Evenki, and along with the Negidals, were classified as Tungus, prior to 1931 (West 2009). The Evens compose most of the Tungus-speakers who migrated to eastern Sakha Republic, along the Kolyma River, and north of the Sea of Okhotsk. According to linguists, the divergence of the Evens from the Evenki happened around

1500 years ago, most likely when Turkic peoples began moving and displaced the Evens and Evenki from their homeland around Lake Baikal (Forsyth 1992; Levin and Potapov 1964; West 2009).

Koryaks

The Koryaks are an indigenous people of Siberia and the Far East of Russia. They are native to the Kamchatka Peninsula and the Koryak Range to the north. The Koryaks were first commented on by the Russians in a travel book written in 1755. However, they are likely the descendants of the first Neolithic inhabitants of the region and therefore its oldest population (West 2009). The Koryaks have close relations with their neighbors – the Chukchi, Evens, Itelmens, and Yukaghirs (Levin and Potapov 1964).

Negidals

Based on genetic analyses, the Negidals may be the last remnants of a culture in the southern Okhotsk region that was centered on the hunting of small sea mammals (Starikovskaya et al. 2005). In the late 1800s, the Negidals lived in small settlements spread along the Amgun and Tugur Rivers, which flow into the Sea of Okhotsk in the Far East region of Russia. Later, they began to mix with and were influenced by the expanding Evenki and Even groups, and today speak a dialect that belongs to the Tungusic language group (Levin and Potapov 1964; Starikovskaya et al. 2005).

Nivkhi

The Nivkhi live on the lower portions of the Amur River and adjacent areas, as well as in the northern part of Sakhalin. They speak a language that is quite distinctive

from their neighbors, who speak languages of the Tunguso-Manchurian group (Levin and Potapov 1964; Starikovskaya et al. 2005). In the Lower Amur Basin, the Nivkhi are considered the most direct descendants of an original Neolithic population of this territory that left many remnants of clay vessels decorated with spiral patterns and human faces (Forsyth 1992; Levin and Potapov 1964).

Udegey

The Udegey live along the slopes of the Sikhote-Alin mountain range in the Primorsky and Khabarovsk Krais, Russia (Levin and Potapov 1964; Starikovskaya et al. 2005). They are the indigenous population of this region and lived in near isolation here until the 19th century (Forsyth 1992). The Udegey language is a part of the southern branch of the Tungusic language group (Levin and Potapov 1964; Starikovskaya et al. 2005).

Ulchi

The Ulchi live primarily in Ulchsky District of Khabarovsk Krai in the Far East region of Russia. Their settlements are located along the Amur River. They speak the Ulchi language, which is close to that of the Nanay, and is regarded by some as a dialect of Nanay. The Ulchi refer to themselves as Nani, while 14th-century Chinese scholars call them and the Nivkhi "Ki-la-mi." Russian sources from the 17th and 18th centuries refer to both the Ulchi and Nivkhi as "Gilyaks." Based on Soviet ethnography, the Ulchi appear to be of mixed origin, and clans have been found to be related to the Evenks, Nanay, Negidals, Nivkhi, Oroks, and Udegeys, as well as clans of Ainu, Manchurian,

and Mongol origin. Culturally, the Ulchi are the most similar to the Nivkhi (Levin and Potapov 1964).

Yukaghir

The Yukaghir live in the basin of the Kolyma River in northeastern Siberia. Geographically, they are divided into two groups: the taiga Yukaghirs living in the Upper Kolyma region of the Sakha Republic and in Srednekansky District of Magadan Oblast and the tundra Yukaghirs who reside in the Lower Kolyma region of the Sakha Republic (Kolga et al. 2001). Between the 17th and 19th centuries, the number of Yukaghirs declined dramatically as the result of war, epidemics, and Tsarist colonial policy, as well as assimilation with the Evens and Yakuts (Kolga et al. 2001; Levin and Potapov 1964).

The Yukaghir language belongs to the Paleo-Asiatic group, and it has been hypothesized that it is related to the Uralic languages; although, this is debated (Levin and Potapov 1964). The name "Yukaghir" was borrowed by Russians from the Yakuts and has a Tungusic origin. The tundra Yukaghirs refer to themselves as Odul, while the taiga Yukaghirs call themselves by their clan names. The origins of the Yukaghir are not known, but excavations carried out by A.P. Okladnikov in the Kolyma region have uncovered an Eastern Siberian Neolithic culture, which can be regarded as the ancestors of the Yukaghirs (Kolga et al. 2001; Levin and Potapov 1964).

TABLE 10. *North/East Asia Sample Composition*

Population/Location	N	Reference	Label/Collection Location
Chukchi	7	Derenko et al. (2007)	Chukchi
	8	Ingman and Gyllensten (2007)	Chukchi
	1	Ingman et al. (2000)	From Chukchi individual
	1	Sukernik et al. (2012)	Russia: Chukchi
	3	Volodko et al. (2008)	Chukchi individual
Even	5	Derenko et al. (2010)	Even
	1	Derenko et al. (2007)	Even
	7	Sukernik et al. (2012)	Even
Koryak	5	Derenko et al. (2010)	Koryak
	6	Derenko et al. (2007)	Koryak
	4	Ingman and Gyllensten (2007)	Koryak
	1	Starikovskaya et al. (2005)	KoriakC2b
	3	Mishmar et al. (2003)	Koryak
Negidal	1	Starikovskaya et al. (2005)	NegidalB5
	2	Mishmar et al. (2003)	Negidal
	3	Volodko et al. (2008)	Negidal individual
Nivkhi	20	Duggan et al. (2013)	Russia: Nivkh
Udegey	1	Mishmar et al. (2003)	Udegey
	1	Sukernik et al. (2012)	Udegey
	18	Duggan et al. (2013)	Udihe
Ulchi	3	Starikovskaya et al. (2005)	Ulchi
	11	Sukernik et al. (2012)	Ulchi individual
Yukaghir	7	Sukernik et al. (2012)	Yukaghir
	13	Volodko et al. (2008)	Yukaghir individual
	132		

South Asia

Two populations were sampled from this geographic area. The populations sampled include: India and Nepal (Table 11). Table 11 includes the sample size, the

references from which the samples were collected, and the label(s) given by the researchers who submitted the sequences to GenBank.

Indians

The Republic of India is a multi-ethnic country in South Asia bordered by multiple bodies of water and adjacent countries. The Indian mtDNA sequences utilized in the present study were originally collected by Kumar et al. (2009) and come from 4 "relic" tribes in north India. The tribes sampled include: Dirang Monpa, Gallong, Lepcha, and Wanchoo. All are indigenous tribes of India that have been recognized as Scheduled Tribes, a term that formally recognizes to some degree indigenous groups (Danver 2013).

Nepalese

Nepal is a landlocked country located between India and the Asian mainland. The population of Nepal is comprised of 125 ethnic groups. Because Nepal is such a diverse country, the Nepalese do not equate their nationality with ethnicity (Cole et al. 2017). The first recorded tribe in Nepal was the Kirats, a Tibeto-Burmese group that came to the area around 2,500 years ago. Initially, the Kirats lived in Kathmandu, but had to move to the high altitude region of the Khumbu valley, Eastern Nepal, in the 4th century after invasion by the Licchavais, an Indian clan (Cole et al. 2017; Gulia 2007).

Since that time Nepal has been exposed to influences form the north and south. Indo-Aryan peoples from northern India form the majority and are represented by the Newar, Pahari, Tarai, and Tharus. Other ethnic groups including the Bhutia, Gurung,

Limbu, Magar, Rai, Sanwar, Sherpa, and Tamang currently reside in Nepal and have links to Turkic immigrants from Central Asia (MacKenzie 2005).

TABLE 11. *South Asia Sample Composition*

Population/Location	N	Reference	Label/Collection Location
India	4	Kumar et al. (2009)	India: Wanchoo
	2	Kumar et al. (2009)	India: Dirang Monpa
	4	Kumar et al. (2009)	India: Lepcha
	10	Kumar et al. (2009)	India: Gallong
Nepal	2	Pala et al. (2012)	Nepal
	17	Fornarino et al. (2009)	Nepal
	1	Wang et al. (2012)	Nepal: Kathmandu
	40		

South/Central Asia

Three populations were sampled from this geographic area. The populations sampled include: Afghanistan, Pakistan, and Tibet (Table 12). Table 12 includes the sample size, the references from which the samples were collected, and the label(s) given by the researchers who submitted the sequences to GenBank.

Afghans

Afghanistan is a landlocked country in south Central Asia. It borders China, Iran, Pakistan, Tajikistan, Turkmenistan, and Uzbekistan. The development of a national identity in Afghanistan is tied to the history and growth of an ethnic identity within the country's Pashtun majority. Originally, the name Afghan was synonymous with Pashtun

and only began to denote citizens of the state in 1747, after the formation of the Kingdom of Afghanistan (West 2009). The origin of Afghans is unclear, but some suggest that they can trace their origin to the Hindu Kush mountain range, and that they initially migrated in batches to Kashmir via Baramulla as the result of intertribal warfare (Khanam 2005).

Pakistanis

Pakistanis are the people who reside in Pakistan, a multi-ethnic country in South Asia. It is bounded by Afghanistan, China, India, and Iran, and has coastline along the Arabian Sea and the Gulf of Oman. Pakistanis belong to seven main linguistic groups: Baloch, Kashmiri, Pashtun, Punjabi, Saraiki, and Urdu, with substantial numbers of other minority language groups as well. Pakistan is inhabited by a wide range of ethnic groups. The Punjabi are the largest ethnic group in Pakistan followed by the Pashtun, who reside in the northwest region. The southeast area of the country is primarily inhabited by the Sindhi. Regional groups like the Saraiki live in the region between Punjab and Sindh. The Kashmiri people live in the north in the Kashmir region. Indigenous groups like the Balti, Hunzakots, and Gilgit live in the northern territories, which were traversed by the Silk Road. There are many other ethnic groups in Pakistan including Bengali, Burmese, and Hazara peoples (Lieven 2011).

Tibetans

The Tibetans are the majority people of Tibet, an autonomous region of China located in the Himalayas in East Asia (MacKenzie 2005). The Tibetans cannot be traced to a single ethnic origin, but are genetically most similar to other East Asian populations.

Additionally, they are more genetically similar to Central Asians than to Siberian populations (Lu et al. 2016). The Tibetan language is a member of the Sino-Tibetan language family. Tibetans were first recorded in the 2nd century BCE by Chinese writers, who referred to them as "Qiang." They lived on the steppes northeast of China at that time and migrated into modern day Tibet in the 1st millennium (MacKenzie 2005).

TABLE 12. *South/Central Asia Sample Composition*

Population/Location	**N**	**Reference**	**Label/Collection Location**
Afghanistan	98	Irwin et al. (2010)	Individual with ancestry from Afghanistan
Pakistan	5	Achilli et al. (2005)	Pakistan
Tibet	20	Ji et al. (2012)	Tibetan
	123		

CHAPTER VI

METHODS

This chapter summarizes the methods used to analyze the genetic data collected for this study.

Data Compilation

To examine the population structure and history of Central Asia, I compiled genetic data from the maternally inherited (mtDNA) genomic system. I downloaded mtDNA sequences from GenBank, an open access collection of publicly available nucleotide sequences. Mitochondrial DNA has a long history of use in phylogeographic reconstruction (Avise 1986; Avise et al. 1979) and is especially useful for reconstructing both population structure and history (Bertranpetit et al. 1995; Comas et al. 1998). Mitochondrial DNA is conservative in size (in humans, 16,569 base pairs), gene content (in humans, 37 genes), and gene arrangement, yet it evolves at a rapid rate at the nucleotide sequence level (Avise et al. 1979). Brown et al. (1979) were the first to record that the rate of mtDNA evolution is 5 to 10 times higher than that of nuclear DNA; and most mtDNA variants can be viewed as neutral markers of the female lineages in which they are found (Avise et al. 1979; Gerber et al. 2001).

Because the entire mtDNA molecule is inherited from the mother, segregation and recombination during sexual reproduction do not introduce new variation and thus muddle attempts at the reconstruction of mtDNA phylogeny (Avise et al. 1979; Calafell

et al. 2000). In fact, the only mechanism that generates new variation in mtDNA is mutation (Calafell et al. 2000). As such, an individual's mtDNA genome contains relatively unambiguous information about the female lineage to which it belongs (Avise et al. 1979). In addition because of the nature of inheritance of mtDNA, individual haplotypes can be fairly easily inferred (Calafell et al. 2000).

The high mutation rate of mtDNA creates variation that can be used in reconstructing population structure and history. In fact, there are recognizable mutation events that occurred after the major continental groups split. Therefore, most mtDNA lineages can be traced to a broad continental origin (Behar et al. 2012; Calafell et al. 2000).

As mentioned in the previous chapter, for this study mtDNA control region sequences were downloaded from GenBank, an open access collection of DNA sequences. The mtDNA sequences were found by first reviewing the literature to locate accession numbers, and then searching GenBank directly using accession numbers when possible, if not geographic locations, author names, and populations were used.

For all populations sampled (see Table 1), I attempted to include a minimum of 20 DNA sequences, but in some cases this was not possible. In total, I assembled a sample of 4,169 mitochondrial control regions from 76 populations. The populations sampled and sample numbers can be seen in Table 1. I have also included a complete list of all DNA sequences downloaded along with GenBank accession numbers and references in Appendix A.

Sequence Alignment

Mitochondrial DNA sequences were aligned using MAFFT version 7, a multiple sequence alignment program (Katoh et al. 2002; Katoh et al. 2017; Katoh and Standley 2013). Multiple sequence alignment (MSA) has an important role in the evolutionary study of DNA sequences (Katoh and Standley 2013). MSA is an algorithmic solution for the alignment of related sequences that takes into account evolutionary events like deletions, insertions, point mutations, and rearrangements (Chatzou et al. 2016). As such, MSA can be used to infer the evolutionary history of related sequences (Katoh et al. 2002).

MAFFT is a freely available MSA program that has been shown to be both accurate and fast, especially when aligning large sets of DNA sequences (Katoh and Standley 2013). A multiple sequence alignment aligns three or more homologous sequences by inserting gaps of varying length within the sequences so that the resulting sequences all have the same length; i.e., so that homologous positions are aligned with one another (Bawono et al. 2017; Chatzou et al. 2016). I used the default settings for MAFFT, which utilizes a progressive method called FFT-NS-2. FFT-NS-2 makes use of a progressive alignment protocol, which constructs an approximate phylogenetic tree for the sequences that is then used to complete the MSA (Pirovano and Heringa 2008). In MAFFT, Fast Fourier Transformation (FFT) is used to quickly identify homologous segments, which are then used to construct the guide tree (Katoh and Standley 2013; Bawono et al. 2017). The guide tree decides the order in which the sequences will be incorporated into the MSA (Chatzou et al. 2016). From there, MAFFT builds the MSA

by adding sequences in the order specified by the guide tree. In FFT-NS-2, MAFFT first builds a quick and dirty guide tree and compiles a corresponding MSA. Then, that MSA is used to construct a more reliable guide tree, which is then used to produce the final MSA (Bawono et al. 2017; Katoh et al. 2002; Katoh and Standley 2013; Pirovano and Heringa 2008).

After the MSA was completed, I visually assessed and edited the alignments, when applicable, using Mesquite 3.10 (Maddison and Maddison 2016). Multiple alignment editors, like Mesquite, are widely used to improve generated alignments manually (Bawono et al. 2017).

MtDNA Haplogroup Classification

Haplogroups were assigned for each sequence using a free web application called HaploGrep 2.0 (Kloss-Brandstätter et al. 2011; Weissensteiner et al. 2016). HaploGrep is based on the latest version of PhyloTree (PhyloTree Build 17), an mtDNA classification tree that is estimated from worldwide data (van Oven 2015). Haplogroup classification is based on the phylogenetic stability of mtDNA polymorphisms, and any range of the mitochondrial genome can be utilized (van Oven 2015; Weissensteiner et al. 2016). For this study, I used the mtDNA control region.

Data Analysis

To investigate the population structure and population history of Central Asia, several tests of intrapopulation and interpopulation variation were utilized. The

calculation of intrapopulation variation included several measures: haplotype diversity, nucleotide diversity, and the mean number of pairwise differences within each population. The calculation of the above measures of intrapopulation variation was used to answer the following questions of interest: 1) how is genetic variation patterned in Central Asia? and 2) how has population history influenced the distribution of genetic variation that is seen in modern-day Central Asian populations? There were two specific questions asked as a part of the latter question that relate to the calculation of the above measures: 1) have Indo-European-speaking groups (Tajiks) been replaced by Turkic-speaking groups (Kazakhs, Kyrgyz, Turkmen, and Uzbeks) throughout Central Asia? and 2) did the cultural "Russification" of Kazakhs leave any traces in the mtDNA?

Haplotype and nucleotide diversity are both measures of genetic variability. High levels of haplotype and nucleotide diversity indicate old, large, and admixed populations, while low levels of these measures indicate young, small populations that may have experienced population bottlenecks. If there is evidence of replacement of Tajiks by Turkic-speaking groups, low levels of haplotype and nucleotide diversity are expected in the Tajik sample. However, this must be weighed against the fact that Tajiks are the oldest residents of Central Asia, which may contribute to high levels of genetic diversity in this population. Kazakhs should have high levels of haplotype and nucleotide diversity if they have had a higher degree of admixture with Russians than other Central Asian populations.

The calculation of the mean number of pairwise differences within each sample provides a measure of the degree of relatedness of sequences. This is of particular

interest in exploring the question of the levels of genetic variation present within Central Asia. If the populations in Central Asia are large, admixed, or old, then the mean number of pairwise differences within each population should be high.

To explore the genetic structure of populations in Central Asia, analysis of molecular variance (AMOVA) was performed. The purpose of the current study is partly to quantify the population structure of Central Asia to examine where this region fits in worldwide models of the distribution of genetic variation. AMOVA was performed in two configurations: 1) populations considered as a single group and 2) populations grouped by major geographic region. The second AMOVA was utilized to test whether geographic structure is a major contributing factor in levels of genetic variation. In addition, genetic distances were calculated between populations to examine population level differences. This was used to examine which populations are more or less similar to each other and answer the following questions:

1) Did Turkic-speaking groups (Kazakhs, Kyrgyz, Turkmen, and Uzbeks) largely replace Indo-European-speaking groups (Tajiks) in Central Asia? If this is the case, then higher genetic distances between Tajiks and other Central Asian populations is expected.
2) Are Uzbeks and Kazakhs more closely related to one another than either is to other Central Asian populations? Because Uzbeks and Kazakhs only recently separated into distinct ethnic groups, a small genetic distance is predicted between these two populations.

3) Are Kazakhs closely related to Russians because of increased cultural assimilation? If the cultural "Russification" of Kazakhs has contributed to their present genetic variation, then the genetic distance between Kazakhs and Russians should be smaller than between Russians and other Central Asian populations.

The calculation of genetic distance was also used to construct a distance matrix that was used in principal component analysis (PCA) to visualize the distribution of genetic diversity between populations.

Calculation of Intrapopulation Variation

Following alignment, sequences were uploaded to Arlequin version 3.5.2 and several measures of intrapopulation diversity were calculated (Excoffier and Lischer 2010). The measures calculated included: haplotype diversity, nucleotide diversity, and the mean number of pairwise differences within each population.

Haplotype diversity (H) is a useful measure of genetic variation and provides information on the structure and history of a population (Chaix et al. 2007; Kousathanas et al. 2017). Nei (1973) quantified gene diversity, which is the probability that within a population two randomly chosen genes are different. This probability is equivalent to heterozygosity in a diploid population that is randomly mating. Therefore, in terms of gene frequencies, gene diversity can be defined in the same way as heterozygosity (Nei 1987). Gene diversity can be used for any organism or gene, whether it is haploid or diploid and is simply a measure of genetic variability (Nei 1973; Nei 1987). The term

haplotype diversity is widely used in the literature, which is why I have chosen to use it here rather than gene diversity or heterozygosity (Garg and Mishra 2018; Kapil et al. 2018).

Haplotype diversity and its variance are calculated according to the following formulas

$$\hat{H} = \frac{n}{n-1}(1 - \sum_{i=1}^{k} p_i^2)$$

$$V(\hat{H}) = \frac{2}{n(n-1)}\left\{2(n-2)\left[\sum_{i=1}^{k} p_i^3 - (\sum_{i=1}^{k} p_i^2)^2\right] + \sum_{i=1}^{k} p_i^2 - (\sum_{i=1}^{k} p_i^2)^2\right\},$$

where n is the sample size, k is the number of haplotypes, and p_i is the sample frequency of the i-th haplotype (Excoffier and Lischer 2010). Haplotype diversity ranges from 0, in populations with little sequence variation, to close to 1.0, in populations with a large number of equally frequent alleles. In general, low haplotype diversity indicates severe effects of small population size (e.g., population bottlenecks), while high haplotype diversity indicates the presence of high levels of genetic variability (Relethford 2012; Silva et al. 2017; Wright 1921; Wright 1969).

Nucleotide diversity (π) is a measure of genetic variation, and is specified as the average number of nucleotide differences per site between two sequences (Nei and Li 1979). Arlequin computes nucleotide diversity as the probability that two randomly homologous sites are different. The formulas for nucleotide diversity and its variance are as follows:

$$\hat{\pi}_n = \frac{\sum_{i=1}^{k} \sum_{j<i} p_i p_j \hat{d}_{ij}}{L}$$

$$V(\hat{\pi}_n) = \frac{n+1}{3(n-1)L}\hat{\pi}_n + \frac{2(n^2+n+3)}{9n(n-1)}\hat{\pi}_n^2$$

where d_{ij} is an estimate of the number of mutations since the divergence of haplotypes i and j, k is the number of haplotypes, p_i is the frequency of haplotype i, n is the sample size, and L is the number of loci (Excoffier and Lischer 2010; Nei 1987; Tajima 1983).

The amount of nucleotide diversity can provide important information on the evolutionary history of a population. This includes data on the effects of social structure on genetic diversity, patterns of migration in the past, signatures of previous selection events, and changes in population size (Yu et al. 2004). Larger, older, and admixed populations as well as those that have not experienced bottlenecks will have higher levels of nucleotide diversity; while populations that are smaller, younger, and closed to gene flow will have low nucleotide diversities (Calafell et al. 2000).

The mean number of pairwise differences within a population is another measure of genetic diversity commonly calculated (Al-Araimi et al. 2017; Calafell et al. 2000; Hong et al. 2015). The mean number of pairwise differences is defined as the average number of differences between all pairs of haplotypes in the sample. The formula used for calculation is:

$$\hat{\pi} = \frac{n}{n-1}\sum_{i=1}^{k}\sum_{j=1}^{k} p_i p_j \hat{d}_{ij},$$

where d_{ij} is an estimate of the number of mutations having occurred since the divergence of haplotypes *i* and *j*, *k* is the number of haplotypes, p_i is the frequency of haplotype *i*, and *n* is the sample size (Excoffier and Lischer 2010). If no recombination and selective neutrality are assumed, the variance is obtained following this formula:

$$V(\hat{\pi}) = \frac{3n(n+1)\hat{\pi} + 2(n^2+n+3)\hat{\pi}^2}{11(n^2-7n+6)}.$$

Arlequin calculates the standard deviation as s.d.(π) = $\sqrt{V(\pi)}$ (Excoffier and Lischer 2010; Tajima 1983; Tajima 1993).

As mtDNA accumulates mutations over time, the number of nucleotide positions at which two sequences differ, the mean number of pairwise differences, provides a measure of the degree of relatedness of the two sequences. This can be applied to a sample of populations and can give an estimate of the relative age at which a population expanded (Calafell et al. 2000). For example, the highest means are found in African populations (Harpending et al. 1993), and this has been used as an argument in favor of the replacement hypothesis for the origin of *Homo sapiens*. For the current study, the calculation of the mean number of pairwise differences was used to assess the relative age of Central Asian populations as compared to that of neighboring populations.

Calculation of Interpopulation Variation

The genetic structure of populations was examined by analysis of molecular variance (AMOVA) using the Arlequin statistical package version 3.5.2 (Excoffier and Lischer 2010). The AMOVA approach used in Arlequin (Excoffier et al. 1992) is similar

to approaches based on analysis of variance of gene frequencies as first defined by Cockerham (1969); (1973) and extended by Weir and Cockerham (1984) and Long (1986); however, it also considers the number of mutations between molecular haplotypes (Excoffier and Lischer 2010).

I ran AMOVA in two different configurations. First, I ran it considering the populations as single groups, and then I performed a second AMOVA, in which populations were grouped by major geographic region as defined in Chapter V. If groups of populations are defined, then a particular genetic structure is being tested. In this case, I am testing whether there is a discernible level of genetic variation that can be attributed to geographic distance as defined by geographic region. A hierarchical analysis of variance separates the total variance into covariance components based on intra-individual differences, inter-individual differences, and/or interpopulation differences (Excoffier 2003; Excoffier and Lischer 2010; Rousset 2000; Weir 1996). The variance components (σ_i^2's) are then used to calculate fixation indices; defined first by Wright (1951) and (1965) in terms of inbreeding coefficients and later, in terms of coalescent times, by Slatkin (1991).

In the case of mtDNA, which is a haploid gene, Arlequin's implementation of AMOVA assumes the *i*-th haplotype frequency vector from the *j*-th population in the *k*-th group is a linear equation of the form

$$\mathbf{x}_{ijk} = \mathbf{x} + \mathbf{a}_k + \mathbf{b}_{jk} + \mathbf{c}_{ijk} ,$$

where the vector **x** is the unknown expectation of $\mathbf{x_{ijk}}$, averaged over the whole study. The effects are **a** for group, **b** for population, and **c** for haplotypes within a population

within a group. These effects are assumed to be independent, additive, and random, and to have the associated covariance components σ_a^2, σ_b^2, and σ_c^2, respectively (Excoffier and Lischer 2010). Thus, the total molecular variance (σ^2) is the sum of the covariance component due to differences among the **G** populations (σ_a^2), the covariance component due to differences among haplotypes in different populations within a group (σ_b^2), and the covariance component due to differences among haplotypes within a population (σ_c^2) (Excoffier and Lischer 2010).

For my first AMOVA run, where populations were treated as single groups, the form of the algorithm implemented in Arlequin results in a fixation index (F_{ST}), which is the same as the weighted average F-statistic over loci (θ_w) defined by Weir and Cockerham (1984). This F_{ST} can be expressed as

$$F_{ST} = \frac{f_0 - f_1}{1 - f_1} = \frac{\bar{t}_1 - \bar{t}_0}{\bar{t}_1},$$

where f_0 is the probability of identity by descent of two different genes drawn from the same population, f_1 is the probability of identity by descent of two genes drawn from two different populations, t_1 is the mean coalescence time of two genes drawn from two different populations, and t_0 is the mean coalescence time of two genes drawn from the same population (Excoffier and Lischer 2010; Michalakis and Excoffier 1996; Slatkin 1991).

A non-parametric permutation approach is used to test the significance of the calculated fixation indices (Excoffier et al. 1992). It consists of permuting haplotypes, individuals, or populations, among individuals, populations, or groups of populations

(Excoffier and Lischer 2010). After each round of permutation, all statistics are recomputed and a null distribution is calculated. Following this procedure, it is not necessary to assume normality (typically assumed for analysis of variance tests) or equality of variance among populations or groups of populations (Excoffier and Lischer 2010). I set the permutation number at 1,000 as Excoffier and Lischer (2010) suggest that a large number of permutations (at least 1,000) is necessary to obtain an accurate final probability and this is a common selection in similar studies (Belledi et al. 2000).

Arlequin implements several different types of hierarchical AMOVA (Excoffier and Lischer 2010). I utilized two of these implementations: 1) AMOVA with haplotypic data and one group of populations and 2) AMOVA with haplotypic data and several groups of populations. Before I explain the way the total sum of squares is separated, how the F-statistics and covariance components are calculated, and which permutation procedures are utilized, it is necessary to define some variables:

TABLE 13. *Definition of AMOVA Variables*

SSD(T)	Total sum of squared deviations.
SSD(AG)	Sum of squared deviations among groups of populations.
SSD(AP)	Sum of squared deviations among populations.
SSD(WP)	Sum of squared deviations within populations.
SSD (AP/WG)	Sum of squared deviation among populations within groups.
G	Number of groups in the structure.
P	Total number of populations.
N	Total number of gene copies in population **p**.
N_p	Number of gene copies in population **p**.
N_g	Number of gene copies in group **g**.

Adapted from (Excoffier and Lischer 2010)

For the AMOVA with haplotypic data and one group of populations, Table 14 and the following formulas define the way the total sum of squares is partitioned and how the covariance components and F-statistics were calculated.

TABLE 14. *AMOVA with Haplotypic Data, One Group of Populations*

Source of variation	Degrees of freedom	Sum of squares (SSD)	Expected mean squares
Among populations	P – 1	SSD(AP)	$n\sigma_a^2 + \sigma_b^2$
Within populations	N – P	SSD(WP)	σ_b^2
Total	N – 1	SSD(T)	σ_T^2

Adapted from (Excoffier and Lischer 2010)

$$n = \frac{N - \sum_p \frac{N_p^2}{N}}{P-1},$$

$$F_{ST} = \frac{\sigma_a^2}{\sigma_T^2}.$$

The permutation procedure for testing F_{ST} and σ_a^2 is performed by permuting haplotypes among populations (Excoffier and Lischer 2010).

For the AMOVA with haplotypic data and several groups of populations, Table 15 and the following formulas define the way the total sum of squares is partitioned and how the covariance components and F-statistics were calculated.

TABLE 15. *AMOVA with Haplotypic Data, Several Groups of Populations*

Source of variation	Degrees of freedom	Sum of squares (SSD)	Expected mean squares
Among groups Among populations / Within groups	G – 1 P – G	SSD(AG) SSD(AP/WG)	$n''\sigma_a^2 + n'\sigma_b^2 + \sigma_c^2$ $n\sigma_b^2 + \sigma_c^2$
Within populations	N – P	SSD(WP)	σ_c^2
Total	N – 1	SSD(T)	σ_T^2

Adapted from (Excoffier and Lischer 2010)

$$S_G = \sum_{g \in G} \sum_{p \in g} \frac{N_p^2}{N_g}, \quad n = \frac{N - S_G}{P - G},$$

$$n' = \frac{S_G - \sum_{p \in P} \frac{N_p^2}{N}}{G - 1}, \quad n'' = \frac{N - \sum_{g \in G} \frac{N_g^2}{N}}{G - 1}$$

$$F_{CT} = \frac{\sigma_a^2}{\sigma_T^2}, \quad F_{SC} = \frac{\sigma_b^2}{\sigma_b^2 + \sigma_c^2} \quad \text{and} \quad F_{ST} = \frac{\sigma_a^2 + \sigma_b^2}{\sigma_T^2}$$

The permutation procedure for testing F_{ST} and σ_c^2 is performed by permuting haplotypes among populations among groups. F_{SC} and σ_b^2 are tested by permuting haplotypes among populations within groups. Lastly, F_{CT} and σ_a^2 are tested by permuting populations among groups (Excoffier and Lischer 2010).

In addition to the AMOVA, I calculated genetic distances between populations using the Arlequin statistical package (Excoffier and Lischer 2010; Gaggiotti and Excoffier 2000). In Arlequin, the pairwise F_{ST} values can be used as genetic distances between populations when a transformation to linearize the distance with population

divergence time is applied (Reynolds et al. 1983). The calculated genetic distances were output in matrix form, which was utilized for further analysis. Following the hypothesis of no difference between populations, a null distribution of pairwise F_{ST} values is calculated by permuting haplotypes between populations (Excoffier and Lischer 2010). The test returns a p-value based on the proportion of permutations leading to an F_{ST} greater than or equal to the observed F_{ST} (Excoffier and Lischer 2010).

In addition to comparing the genetic distances between populations, the distance matrix was used to perform a principal component analysis (Cavalli-Sforza et al. 1994; Comas et al. 1998; Quintana-Murci et al. 2004) using SPSS 20 (IBM Released 2011). Principal component analysis is a procedure that simplifies multivariate data, but with a minimal loss of data (Cavalli-Sforza and Edwards 1964; Hotelling 1933). In the current study, principal component analysis (PCA) was utilized to produce a visualization of the distribution of genetic diversity between populations. In PCA, the distance matrix is transformed into a correlation matrix in order to calculate the principal components (PCs). By doing this, a non-Euclidean space is generated, which has the potential to create some information loss, but has the advantage of providing evolutionary meaning of genetic distances (Cavalli-Sforza et al. 1994).

For the last interpopulation analysis, SPSS 20 was used to estimate the percentages of mtDNA haplogroups in each population (IBM Released 2011). Using the haplogroup percentage matrix, a PCA was performed to show the clustering patterns of the populations (Yao et al. 2004). By looking at the haplogroups present in Central Asian populations, I was able to assess relationships between them and other

neighboring populations by comparing relative proportions of East and West Eurasian haplogroups. The percentage of haplogroups in Central Asia was also used to provide information on the genetic diversity present in each of the populations sampled from this region.

In order to explore both the population structure and history of Central Asia, measures of intrapopulation and interpopulation variation were calculated. The analyses described above were performed to answer the following questions regarding the genetic similarity between populations in Central Asia as well as with neighboring populations:

1) How is genetic variation within Central Asia patterned?
2) What, if any, geographic barriers have affected population interactions in Central Asia?
3) How has population history influenced the distribution of genetic variation in Central Asian populations?

These analyses are necessary to quantify the genetic variation within Central Asia and to examine Central Asia's place in the worldwide distribution of genetic variation. In order to have a full understanding of genetic variation in *Homo sapiens*, Central Asia must be included and the analyses performed in the current study allow that to be done.

CHAPTER VII

RESULTS

In this chapter, I discuss the results of the mtDNA haplogroup classification as well as the intra- and interpopulation analyses. I will have organized the chapter according to the different analyses conducted. First, I will discuss the results of the mtDNA haplogroup classification. Next, I will discuss the results of the intrapopulation and interpopulation variation analyses.

MtDNA Haplogroup Classification

The maternal genetic ancestry of Central Asian populations was explored by characterizing control region sequences from 1,326 inhabitants of Central Asia, which yielded 417 mtDNA haplogroups. The haplogroups for all individuals sampled from Central Asia are reported in Appendix C. For a complete list of haplogroups for all individuals sampled in this study, see Appendix A. All major haplogroups except E, O, P, Q, and S are represented in Central Asia. The majority of mtDNAs were of either an East or West Eurasian origin; although, there are also mtDNAs of South Asian origin represented.

Haplogroup L1 was found in only two individuals from Uzbekistan. The mtDNA haplogroups L0, L1, L2, L3, L4, L5, and L6 all have an African origin, and all mtDNA haplogroups outside of Africa are the result of divergence from the L3 haplogroup (Soares et al. 2009). The finding of two individuals from Uzbekistan with an L1

haplogroup is thus most likely the result of admixture with individuals with African maternal ancestry. The haplogroup profiles of all populations from Central Asia were very similar with a few exceptions. In the Kazakh sample, haplogroups R9, U3, V, and Y are not represented. For the Kyrgyz sample, R0, R9, and U1 are not found. For the Kazakh and Kyrgyz samples, the haplogroups not found are all diverged from haplogroup N, which is descended from L3 and found primarily in Europe and Oceania (Olivieri et al. 2006). Haplogroups I, M8, M9, N9, R0, U8, V, X2, Y, and Z are not found in Tajikistan. These missing haplogroups represent origins from both haplogroups M and N. Tajikistan showed the lowest diversity in terms of mtDNA haplogroups represented. In the Turkmen sample, haplogroups M8, N1, N9, U8, V, and Z are not represented. Lastly for Uzbekistan, haplogroups M8, R9, and U8 are not represented. The Kyrgyz and Uzbek samples have the highest diversity of mtDNA haplogroups.

Intrapopulation Variation Analyses

As discussed in the previous chapter, summary statistics were calculated to assess the levels of genetic diversity in Central Asian populations. The haplotype diversity, nucleotide diversity, and mean number of pairwise differences for all populations sampled are presented in Table 16. Haplotype and nucleotide diversity are measures of genetic variability. High levels of haplotype and nucleotide diversity indicate admixed, large, or old populations, while the opposite would be true of populations with low levels of haplotype and nucleotide diversity. In this study, these measures were used to answer questions regarding the patterning of genetic variation in

Central Asia. High levels of both haplotype and nucleotide diversity were predicted for the Kazakh sample as the result of increased contact and interaction with Russians, while low levels of both measures were expected for Tajiks because of their history of being forced out of Central Asia or into smaller geographic areas by expanding Turkic-populations.

In general, the haplotype diversity for Central Asian populations is high, ranging from 0.978 (Tajikistan) to 0.999 (Kazakhstan). Most of the 76 populations sampled had high haplotype diversity; although, there are several populations from East Europe and North/East Asia that have lower haplotype diversities than those found in Central Asia including populations from East Europe, Near East, North/East Asia, North/Central Asia, South Asia, and South/Central Asia (Table 16). It is important to keep in mind that the calculation of haplotype diversity is influenced by sample size and so the haplotype diversity for populations with low sample sizes (e.g., Bosnia, Chuvash, Pakistan, etc.) may not be an accurate representation of the genetic diversity in these populations. The levels of nucleotide diversity in Central Asia range from 0.011 (Turkmenistan) to 0.013 (Kazakhstan and Tajikistan). These numbers are in the upper range for nucleotide diversity in this data set, but they are exceeded by populations from East Europe and North/Central Asia (Table 16).

The mean number of pairwise differences within each population is a measure that provides information on the degree of relatedness of sequences. This measure was calculated to examine the levels of genetic variation present in Central Asia. If the populations in Central Asia are admixed, large, or old, then the mean number of pairwise

differences within each population should be high. Previous studies have found that Central Asian populations exhibit high levels of genetic diversity and suggest that these levels are the result of admixture between differentiated gene pools (Comas et al. 1998; Comas et al. 2004; Quintana-Murci et al. 2004). These studies did not use all five Central Asian populations and/or had small sample sizes. Comas et al. (1998) only included individuals from Kazakhstan and Kyrgyzstan, while Quintana-Murci et al. (2004) included only Turkmen and Uzbeks. Comas et al. (2004) did include individuals from all five Central Asian countries, but the sample size was only 20 for each. The present study expands the sample size and includes a representative Central Asian sample and so will be able to more effectively address the question of the levels of genetic variation present in Central Asia.

The results for the mean number of pairwise differences generally match up with the nucleotide diversities. The mean number of pairwise differences in Central Asia range from 12.919 (Turkmenistan) to 14.418 (Tajikistan). When these values are compared with those in other regions, they are generally in the same range as Caucasus South, Near East, North Asia, North/Central Asia, and South/Central Asia; although, some populations within these samples have values that are below or above those found in Central Asia (Table 16). The values in East Asia range from 11.311 (Bargut) to 15.489 (China), while the values in East Europe range from 9.911 (Belarus) to 18.833 (Chuvash). Unlike the findings of Comas et al. (1998), Central Asian populations do not have values that are intermediate between East Asia and Europe. In fact, there is considerable overlap in the mean number of pairwise differences between populations in

all regions. South Asia, represented by India and Nepal, is the only region that has values lower than Central Asia for all populations (Table 16).

TABLE 16. *Haplotype Diversity, Nucleotide Diversity, and Pairwise Differences*

Region	Population	N	Haplotype diversity	Nucleotide diversity	Pairwise differences
Caucasus North	Adygei	4	1.000 ± 0.177	0.011 ± 0.007	12.000 ± 6.906
	Dargin	3	1.000 ± 0.272	0.004 ± 0.003	4.667 ± 3.127
	North Ossetian	14	1.000 ± 0.027	0.013 ± 0.007	14.758 ± 7.033
Caucasus South	Armenia	20	1.000 ± 0.016	0.011 ± 0.006	12.574 ± 5.922
	Azerbaijan	20	0.995 ± 0.018	0.013 ± 0.007	14.300 ± 6.692
	Georgia	20	1.000 ± 0.016	0.011 ± 0.006	12.905 ± 6.070
Central Asia	Kazakhstan	256	0.999 ± 0.001	0.013 ± 0.006	14.047 ± 6.321
	Kyrgyzstan	249	0.996 ± 0.001	0.012 ± 0.006	13.202 ± 5.960
	Tajikistan	244	0.978 ± 0.003	0.013 ± 0.006	14.418 ± 6.482
	Turkmenistan	249	0.990 ± 0.001	0.011 ± 0.006	12.919 ± 5.839
	Uzbekistan	328	0.998 ± 0.001	0.012 ± 0.006	13.516 ± 6.090
East Asia	Bargut	20	1.000 ± 0.016	0.010 ± 0.005	11.311 ± 5.358
	China	377	0.997 ± 0.001	0.013 ± 0.007	15.489 ± 6.932
	Han	16	1.000 ± 0.022	0.012 ± 0.006	13.642 ± 6.471
	Mongolia	9	1.000 ± 0.052	0.013 ± 0.007	14.944 ± 7.392
East Europe	Albania	5	1.000 ± 0.127	0.015 ± 0.009	16.800 ± 9.048

TABLE 16. *continued*

Region	Population	N	Haplotype diversity	Nucleotide diversity	Pairwise differences
East Europe (con't)	Belarus	20	0.963 ± 0.026	0.008 ± 0.005	9.911 ± 4.733
	Bosnia	5	1.000 ± 0.127	0.010 ± 0.007	11.600 ± 6.352
	Bulgaria	20	0.990 ± 0.019	0.010 ± 0.005	11.521 ± 5.452
	Chuvash	4	0.833 ± 0.222	0.017 ± 0.011	18.833 ± 10.644
	Csango	100	0.941 ± 0.016	0.010 ± 0.005	11.886 ± 5.423
	Czech Republic	20	1.000 ± 0.016	0.010 ± 0.005	11.558 ± 5.469
	Estonia	7	1.000 ± 0.076	0.011 ± 0.006	12.190 ± 6.284
	Hungary	211	0.994 ± 0.002	0.009 ± 0.005	10.746 ± 4.911
	Kalmyk	6	1.000 ± 0.096	0.013 ± 0.008	14.200 ± 7.442
	Lithuania	12	0.970 ± 0.044	0.014 ± 0.008	15.773 ± 7.578
	Moldova	4	1.000 ± 0.177	0.009 ± 0.006	10.333 ± 5.993
	Poland	20	0.963 ± 0.033	0.012 ± 0.006	13.163 ± 6.185
	Roma	205	0.914 ± 0.013	0.010 ± 0.005	11.666 ± 5.306
	Romania	17	0.956 ± 0.037	0.011 ± 0.006	11.868 ± 5.652
	Russia	151	0.992 ± 0.003	0.009 ± 0.005	10.547 ± 4.833
	Slovakia	20	0.995 ± 0.018	0.010 ± 0.005	11.289 ± 5.349
	Szekely	178	0.994 ± 0.002	0.011 ± 0.005	12.010 ± 5.457
	Tatar	20	0.995 ± 0.018	0.011 ± 0.006	12.147 ± 5.732
	Ukraine	20	1.000 ± 0.016	0.012 ± 0.007	14.079 ±6.593
Near East	Cyprus	91	0.993 ± 0.003	0.011 ± 0.006	13.032 ± 5.922

TABLE 16. *continued*

Region	Population	N	Haplotype diversity	Nucleotide diversity	Pairwise differences
Near East (con't)	Dubai	12	1.000 ± 0.034	0.013 ± 0.007	14.985 ± 7.216
	Iran	20	0.984 ± 0.024	0.011 ± 0.006	11.968 ± 5.652
	Iraq	182	0.998 ± 0.001	0.012 ± 0.006	13.930 ± 6.280
	Israel	16	0.992 ± 0.025	0.013 ± 0.007	13.858 ± 6.569
	Jordan	12	1.000 ± 0.034	0.010 ± 0.006	11.379 ± 5.557
	Kuwait	381	0.998 ± 0.001	0.013 ± 0.007	15.376 ± 6.883
	Lebanon	20	0.979 ± 0.025	0.010 ± 0.005	11.700 ± 5.532
	Palestine	9	1.000 ± 0.052	0.012 ± 0.007	13.222 ± 6.578
	Saudi Arabia	18	1.000 ± 0.019	0.014 ± 0.007	15.307 ± 7.177
	Syria	6	1.000 ± 0.096	0.011 ± 0.007	12.200 ± 6.440
	Turkey	20	0.995 ± 0.018	0.013 ± 0.007	14.537 ± 6.797
	Yemen	19	0.912 ± 0.061	0.012 ± 0.006	12.982 ± 6.119
North Asia	Evenki	19	0.983 ± 0.022	0.010 ± 0.005	11.310 ± 5.371
	Mansi	12	1.000 ± 0.034	0.012 ± 0.007	13.500 ± 6.533
	Nganasan	12	0.985 ± 0.040	0.010 ± 0.006	11.576 ± 5.647
	Yakut	11	0.982 ± 0.046	0.012 ± 0.006	13.091 ± 6.390
North/Central Asia	Altaian Kazakh	13	0.987 ± 0.035	0.010 ± 0.006	11.705 ± 5.673
	Altaian Kizhi	20	1.000 ± 0.016	0.013 ± 0.007	14.595 ± 6.823
	Buryat	20	0.984 ± 0.024	0.010 ± 0.006	11.742 ± 5.551
	Ket	4	1.000 ± 0.177	0.013 ± 0.009	14.500 ± 8.274

TABLE 16. *continued*

Region	Population	N	Haplotype diversity	Nucleotide diversity	Pairwise differences
North/Central Asia (con't)	Khamnigan	20	0.995 ± 0.018	0.011 ± 0.006	12.142 ± 5.729
	Shor	12	0.970 ± 0.044	0.012 ± 0.007	13.939 ± 6.735
	Teleut	8	1.000 ± 0.063	0.012 ± 0.007	13.179 ± 6.647
	Tofalar	4	1.000 ± 0.177	0.016 ± 0.011	17.667 ± 10.006
	Tubular	20	1.000 ± 0.016	0.015 ± 0.008	16.647 ± 7.738
	Tuvinian	17	0.985 ± 0.025	0.009 ± 0.005	10.485 ± 5.030
	Uyghur	2	1.000 ± 0.500	0.013 ± 0.014	15.000 ± 10.954
North/East Asia	Chukchi	20	0.942 ± 0.030	0.008 ± 0.004	9.458 ± 4.531
	Even	13	0.987 ± 0.035	0.009 ± 0.005	9.641 ± 4.728
	Koryak	19	0.971 ± 0.024	0.009 ± 0.005	10.421 ± 4.973
	Negidal	6	1.000 ± 0.096	0.012 ± 0.007	13.733 ± 7.208
	Nivkhi	20	0.921 ± 0.041	0.006 ± 0.003	6.302 ± 3.120
	Udegey	20	0.890 ± 0.051	0.006 ± 0.003	7.163 ± 3.506
	Ulchi	14	0.989 ± 0.031	0.010 ± 0.006	12.165 ± 5.853
	Yukaghir	20	0.984 ± 0.021	0.009 ± 0.005	10.205 ± 4.865
South Asia	India	20	0.921 ± 0.042	0.005 ± 0.003	6.084 ± 3.023
	Nepal	20	0.995 ± 0.018	0.009 ± 0.005	10.563 ± 5.025
South/Central Asia	Afghanistan	98	0.946 ± 0.014	0.011 ± 0.005	12.144 ± 5.535
	Pakistan	5	1.000 ± 0.127	0.012 ± 0.007	13.000 ± 7.078
	Tibet	20	1.000 ± 0.016	0.011 ± 0.006	12.563 ± 5.917

Interpopulation Variation Analyses

Because the purpose of the current study is to quantify the population structure of Central Asia, analysis of molecular variance (AMOVA) was performed. As discussed in the previous chapter, AMOVA was performed in two configurations - populations considered as a single group and populations grouped by geographic region. This analysis was used to examine the question of whether any geographic barriers may have affected or are continuing to affect population interactions in Central Asia.

The results for the AMOVA with all populations considered as one group are shown in Table 17 and for the AMOVA with populations grouped according to geographic region in Table 18. The F_{ST} for the AMOVA in which all populations are considered as a single group is 0.03680 with a p-value of 0.00, indicating that it is significantly different from 0. F_{ST} values range from 0 to 1, with 0 indicating populations that are randomly mating and 1 indicating that all genetic variation is accounted for by population structure, and the two populations do not share any genetic diversity (Holsinger and Weir 2009; Mosaad et al. 2015; Wright 1931). The percentage of variation within populations is 96.32, while the percentage of variation among populations is 3.68 (Table 17). This result indicates that 3.68% of the genetic diversity can be accounted for by genetic differences among populations and thus the majority of the variation is between individuals within populations.

TABLE 17. *AMOVA – One Group*

Source of variation	**d.f.**	**Sum of squares**	**Variance components**	**Percentage of variation**
Among populations	10	823.55	0.23 (V_a)	3.68
Within populations	4158	25361.25	6.10 (V_b)	96.32
Total	4168	26184.80	6.33	100.00
Fixation Index	F_{ST}:	0.03680		

For the AMOVA with populations grouped according to geographic region, F-statistics were calculated to estimate the proportion of genetic variability found among populations (F_{ST}), among populations within groups (F_{SC}), and among groups (F_{CT}). The F-statistics are F_{ST} = 0.06538, F_{SC} = 0.4139, and F_{CT} = 0.02502 (Table 18). The p-values for all F-statistics were equal to 0.0000, indicating that they are all significantly different from 0. The percentage of variation within populations is 93.46, among populations within groups is 4.04, and among groups is 2.50 (Table 18). This result indicates that 2.5% of the genetic diversity can be accounted for by genetic differences among groups. In summary, mtDNA sequence variation appears to be at least somewhat geographically structured, with 2.5% of the genetic variation accounted for by geographic region.

TABLE 18. *AMOVA – Populations Grouped According to Geographic Region*

Source of variation	**d.f.**	**Sum of squares**	**Variance components**	**Percentage of variation**
Among groups	10	823.55	0.16 (V_a)	2.50
Among populations within groups	65	1150.32	0.26 (V_b)	4.04
Within populations	4093	24210.93	5.92 (V_c)	93.46
Total	4168	26184.80	6.33	100.00
Fixation Indices	F_{SC}: F_{ST}: F_{CT}:	0.04139 0.06538 0.02502		

Genetic distances between Central Asian populations and all other populations were calculated as described in chapter VI. The genetic distance matrix is included in Appendix B. The calculation of genetic distances between populations was performed to examine population level differences and to answer questions about which populations are more or less similar to one another.

In general, the Central Asian populations presented the shortest genetic distances among themselves with a few notable exceptions. For Kazakhstan, the genetic distances between the Central Asian populations ranged from 0.02442 (Tajikistan) to 0.00506 (Uzbekistan). Kazakhstan presented the shortest overall genetic distance with the sample from Bosnia (0.00429). The genetic distance between Kazakhs and Tajiks was greater than that seen between Kazakhs and several other populations outside of Central Asia

including Adygei, Bargut, Ket, Mansi, Moldova, Mongolia, Negidal, and Tuvinian. It was hypothesized that Kazakhs might share genetic affinity with Russians because of increased contact and interaction. In fact, the genetic distance between Kazakhstan and Russia was 0.06151. This genetic distance is higher than that seen between Russia and Uzbekistan, Tajikistan, and Turkmenistan.

For Kyrgyzstan, the highest genetic distance with another Central Asian population was with Tajikistan (0.025) and the lowest was with Kazakhstan (0.00639). Kyrgyzstan demonstrated a shorter genetic distance with two populations – Bargut (0.00585) and Yakut (0.00629). In addition, Kyrgyzstan had shorter genetic distances between Bosnia, Buryat, China, Khamnigan, Mansi, Mongolia, Negidal, Shor, and Tuvinian than it did with Tajikistan.

Within Central Asia, Turkmenistan demonstrated the highest genetic distance with Tajikistan (0.019) and the lowest with Uzbekistan (0.00261). The genetic distance between Turkmenistan and Uzbekistan is the lowest seen when Turkmenistan is compared to any other population. The genetic distance between Turkmen and Tajiks was greater than that seen between Turkmenistan and Altaian Kazakh, Armenia, Iraq, Kalmyk, Kuwait, and Tatar.

For Uzbekistan, the highest genetic distance with another Central Asian population was with Tajikistan (0.01496) and the lowest was with Turkmenistan (0.00261). Uzbekistan had the shortest genetic distance with the Kalmyk (0.00212). The genetic distance between Tajiks and Uzbeks was greater than that seen between Uzbeks and Adygei, Armenians, Kalmyk, Mongolians, and Tatars. Because Uzbeks and Kazakhs

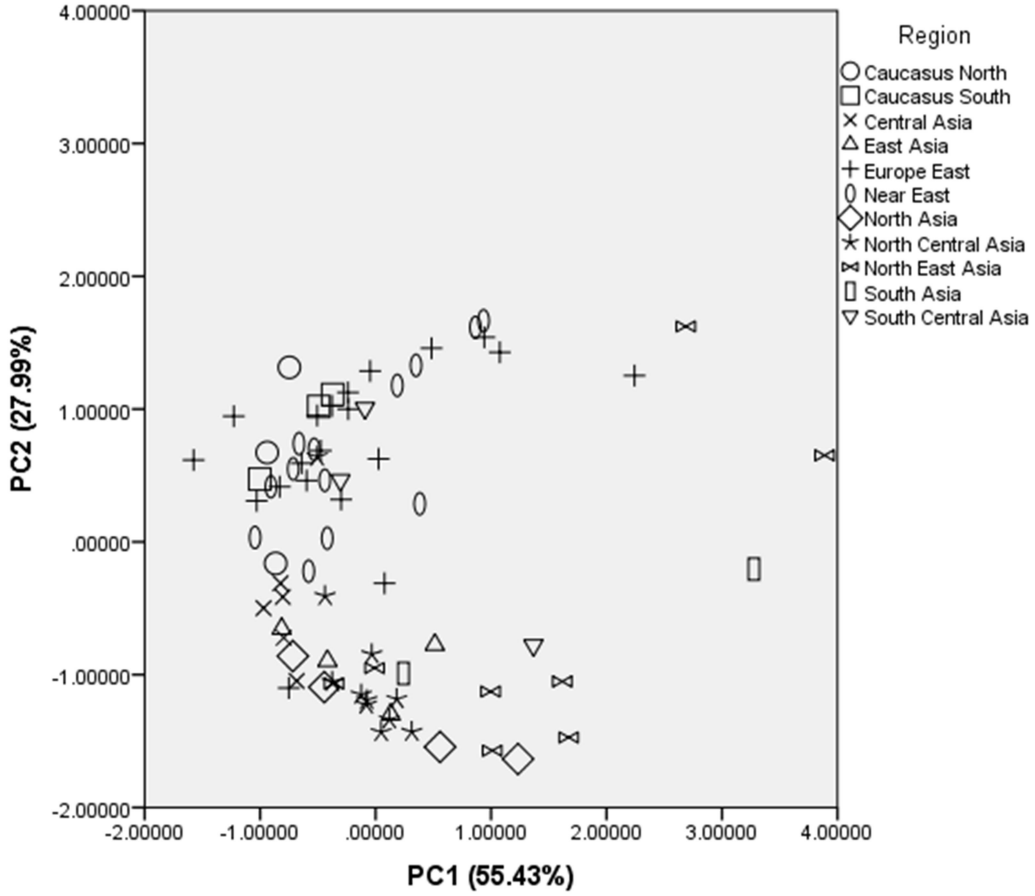
only recently separated into distinct ethnic groups, it was predicted that these two populations would demonstrate a short genetic distance. While Kazakhstan did have the shortest genetic distance with Uzbekistan (0.00506), Uzbekistan had a shorter genetic distance with Turkmenistan (0.00261).

Lastly, when Tajikistan is compared to other Central Asian populations it has the highest genetic distance with Kyrgyzstan (0.025) and the lowest with Uzbekistan (0.01496). Tajikistan had the shortest genetic distances with Bosnia (0.00012) and the Dargin (0.00991). Tajikistan had shorter genetic distances with Armenia, Kalmyk, Moldova, Mongolia, and Tatars than it did with Kyrgyzstan. It was predicted that if Turkic-speaking groups (Kazakhs, Kyrgyz, Turkmen, and Uzbeks) largely replaced Tajiks in Central Asia, higher genetic distances between Tajiks and other Central Asian populations was expected. In Central Asia, all Turkic-speaking populations presented the highest genetic distances with Tajikistan and, in fact, all other Central Asian populations are genetically more similar to one another than any are to Tajiks.

Principal component analysis (PCA) was performed using the genetic distance matrix as described in Chapter VI. PCA allows a visualization of the distribution of genetic diversity between populations. This provides a visual means of assessing population similarities and differences. The results from the PCA using the genetic distance matrix are displayed in Figure 3. In Figure 3, principal component 1 (PC1) is along the x-axis and principal component 2 (PC2) is along the y-axis. PC1 accounts for 55.43% of the genetic variation, while PC2 accounts for 27.99%. Along PC1, all the populations form a fairly tight cluster with the exception of the Chuvash (East Europe),

Indian (South Asia), and Chukchi and Nivkhi (North/East Asia) samples. The Chuvash sample is very small, only four individuals and this could explain its position as an extreme outlier. Both the Chukchi and Nivkhi are indigenous ethnic groups living in the Far East of Russia. They were traditionally nomadic and both have experienced contact with other populations, including Russians. However, it appears that there has not been much admixture, at least in regards to the maternal lineage. Their position in this analysis may be the result of genetic drift as the result of small population size or an isolated gene pool. Lastly, the Indian sample used in this analysis is composed of mtDNA form 4 tribes in North India. I expect that their position may be a reflection of the sample composition rather than a true representation of India's genetic relationship with neighboring populations.

FIGURE 3. *PCA from Genetic Distance Matrix*



For the Central Asian populations, they are all clustered fairly tightly along both PC1 and PC2 (Figure 3). Tajikistan, Turkmenistan, and Uzbekistan form a cluster higher along PC2 with Kazakhstan and then Kyrgyzstan slightly farther down. The Central Asian cluster overlaps with populations from East Asia (Mongolia), East Europe (Kalmyk), and North Asia (Mansi and Yakut). In addition, the Central Asian cluster is close to populations from the Near East, North/Central Asia, and North/East Asia.

Additionally, there is broad separation between the Near East, East Europe, and the Caucasus on the top of the graph and Asia on the bottom with the exception of the Afghanistan and Pakistan samples, which are well outside of the Asian cluster, and the Kalmyk sample, which is within the Asian cluster. The Kalmyk are ancestrally from the Altai region in western Mongolia and migrated to their present-day location in Russia's North Caucasus territory in the 1600s so it is not surprising that they would cluster with other Asian populations. The geographic location of Afghanistan and Pakistan as well as their histories may explain their position in Figure 3.

The percentages of each haplogroup were calculated and a haplogroup percentage matrix was used to perform PCA as described in Chapter VI. The relative proportion of haplogroups was used to assess genetic relationships between Central Asian populations and other populations in this data set. The percentage of haplogroups in Central Asia also provides information on the genetic diversity present within each of the populations sampled from this region. The haplogroup percentages for Central Asian populations are shown in Table 19. For a complete haplogroup table see Appendix D.

For all Central Asian populations except the Kyrgyz, haplogroup H is present at a high frequency (Table 19). Haplogroup H is the most frequent haplogroup in Central Asia (14.48) followed by D4 (10.11) and C (10.03). Haplogroup H is the most common mtDNA haplogroup in Europe, and is also common in the Middle East and North Africa, as well as in Central Asia and northern India, where it maintains frequencies of between 5 and 10% (Achilli et al. 2004). Haplogroup D is thought to have arisen in Asia and is composed of two main branches: D4 and D5'6 (Soares et al. 2009; van Oven 2015).

Relevant to the present study, haplogroup D4 is the most common mtDNA haplogroup in several populations from northeast Asia including the Buryats, Khamnigan, Kalmyks, and Altaian Kazakhs (Derenko et al. 2012; Derenko et al. 2007). It is also seen in populations from Siberia, China, and Central Asia (Comas et al. 2004; Volodko et al. 2008; Wen 2005). Lastly, haplogroup C is frequent among Arctic populations, including the Yukaghir and Nganasan, and is also seen in Central Asia (Comas et al. 2004; Volodko et al. 2008).

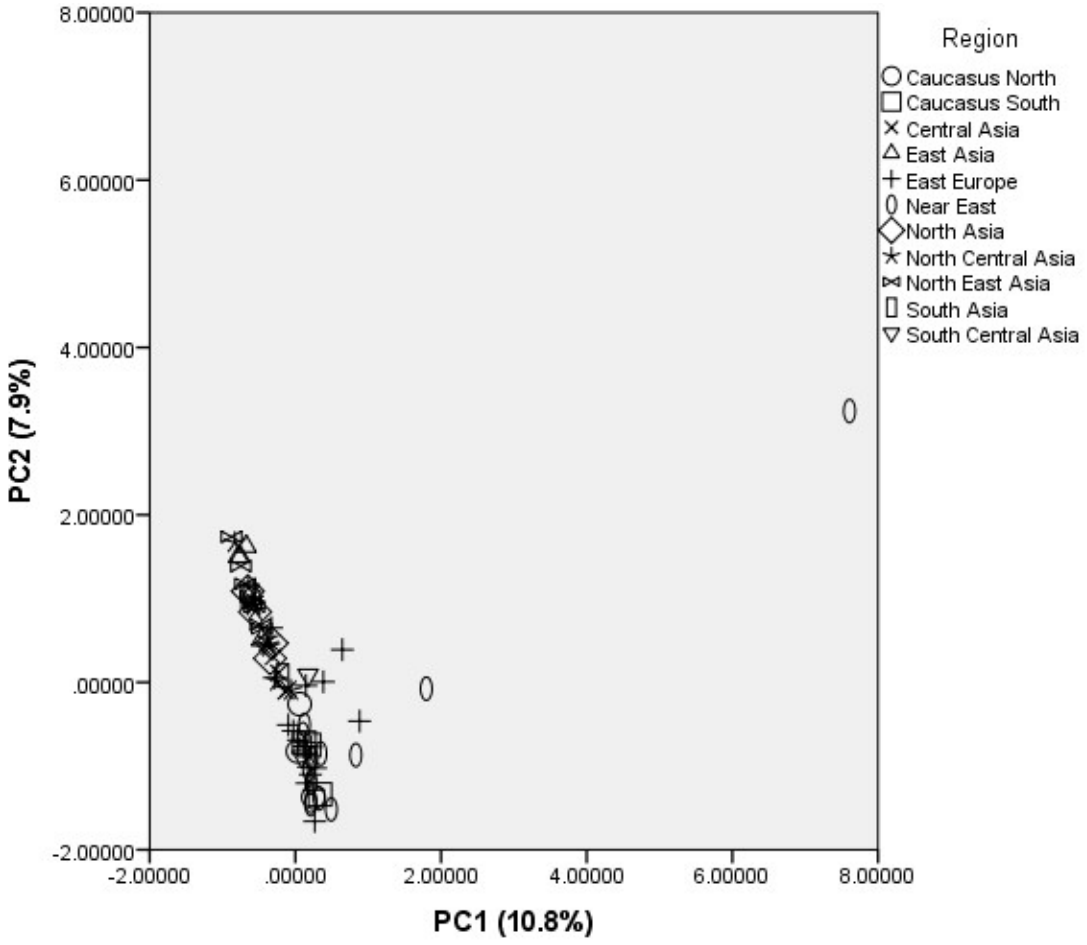
As seen in Table 19 below, Kazakhs have high frequencies of haplogroups D4 (13.67) and H (13.67), Kyrgyz C (12.85) and D4 (14.06), Tajiks C (14.75), F (11.89), and H (11.48), Turkmen H (22.89), and Uzbeks H (16.16). Haplogroup F is seen at much higher frequency in Tajiks than in any of the other Central Asian populations; although, it is present in all. Haplogroup F is most common in East and Southeast Asia (Asari et al. 2007; Comas et al. 2004; Hill et al. 2007). It is found among Han Chinese, Ket, Shor, and Uyghur populations (Comas et al. 2004). Also of interest, two haplogroups, which Comas et al. (2004) identified as expanding from Central Asia – D4c and G2a, were also found in the present study. Haplogroup D4c was found in all Central Asian populations except Tajiks, while G2a was found in all Central Asian populations; although, there is only one individual from Tajikistan with this haplogroup.

TABLE 19. *Central Asian Haplogroup Percentages*

Hg	Kazakh	Kyrgyz	Tajik	Turkmen	Uzbek	Total
#	256	249	244	249	328	1326
A	8.20	5.62	1.64	4.02	3.96	4.68
B	2.34	8.43	0.82	0.80	1.52	2.71
C	7.81	12.85	14.75	6.83	8.54	10.03
D4	13.67	14.06	6.15	8.03	8.84	10.11
D5	1.17	4.02	4.10	0.80	2.13	2.41
F	4.30	2.41	11.89	4.82	2.74	5.05
G	7.03	3.21	0.41	3.61	3.05	3.47
H	13.67	7.63	11.48	22.89	16.16	14.48
HV	3.91	1.20	2.05	0.80	3.96	2.49
I	0.78	1.20		1.61	2.74	1.36
J	3.13	2.81	1.23	7.63	3.66	3.70
K	2.34	0.80	1.64	2.81	3.35	2.26
L1					0.61	0.15
M*	2.73	8.03	5.33	7.63	4.57	5.58
M7	0.78	1.61	1.23	0.40	1.83	1.21
M8	0.78	0.80				0.30
M9	3.13	4.42		0.80	1.52	1.96
N*		0.40		2.41	1.83	0.98
N1	0.78	0.40	1.23		0.91	0.68
N9	1.56	1.20			0.31	0.60
R*	0.39	0.40	0.41	2.81	3.05	1.51
R0	0.39			0.40	0.91	0.38
R9			0.41			0.08
T	5.08	2.41	7.79	5.22	7.01	5.58
U1	0.78		3.28	0.80	0.91	1.13
U2	3.52	0.80	2.05	2.41	2.74	2.34
U3		0.80	2.05	0.80	1.22	0.98
U4	2.34	4.02	0.41	3.61	1.52	2.34
U5	5.47	3.61	9.02	1.61	3.96	4.68
U7	0.78	0.40	4.92	0.80	1.52	1.66
U8	0.39	0.40				0.15
V		0.40			0.30	0.15
W	1.17	1.61	5.74	2.01	1.83	2.41
X2	0.39	0.40		2.41	1.83	1.06
Y		2.41		1.20	0.30	0.75
Z	1.17	1.20			0.61	0.60

As mentioned above, a PCA based on the haplogroup percentage matrix (Appendix D) was run and the results are presented in Figure 4. As shown in Figure 4, all populations cluster very tightly along PC1 with the exception of Kuwait. The Central Asian populations fall in the middle of the clustering along PC2. Along PC2, the Central Asian populations fall below the populations from East Asia and above the populations from East Europe with some slight overlap. In general, the populations follow a west to east clinal pattern, with populations from the west near the bottom, populations from the east near the top, and Central Asia in the middle.

FIGURE 4. *PCA from Haplogroup Percentage Matrix*



To summarize the results of the present study, Central Asia has a high diversity of haplogroups, high haplotype diversity, and relatively high nucleotide diversity as well as mean number of pairwise differences within populations. These results are consistent with previous findings that there is a high level of genetic diversity present in Central Asia (Comas et al. 1998; Comas et al. 2004; Quintana-Murci et al. 2004). I will discuss what I believe has caused this high genetic diversity in the next chapter.

In terms of the interpopulation analyses, the results of the AMOVA have shown that a small portion of genetic variation (2.50%) can be accounted for by geographic region. This does not necessarily indicate any kind of geographic barriers to population interactions and will be discussed in more detail in the next chapter. When examining the genetic distances between populations, Central Asian populations generally exhibit the shortest genetic distances among themselves, with a few exceptions discussed previously. Kazakhstan and Uzbekistan were found to have a short genetic distance; although, Uzbekistan actually had the shortest genetic distance to Turkmenistan. Additionally, it was found that contrary to expectations, the genetic distance between Russia and Kazakhstan was not the shortest among Central Asian populations. Lastly as predicted, Tajikistan showed the largest genetic distance from all other Central Asian populations. The PCA performed based on the genetic distance matrix found that the Central Asian populations clustered together and overlapped with populations from East Asia, East Europe, and North Asia (Figure 3). In addition, they were close to populations from the Near East, North/Central Asia, and North/East Asia. There was also broad separation between the Near East, East Europe, and the Caucasus and Asia.

Finally, Central Asia had the highest percentages of mtDNA haplogroups H, D4, and C, which have high frequencies in Europe, East Asia, and the Arctic, respectively. Two haplogroups, D4c and G2a, suggested to have expanded from Central Asia (Comas et al. 2004) were also found in the present analyses. The PCA from the haplogroup percentage matrix identified an east to west cline of haplogroup frequencies with Central Asia falling in the middle of the distribution (Figure 3). In the next chapter, I will discuss

these findings and answer the questions that I have raised as pertinent in the present study.

CHAPTER VIII

DISCUSSION

I asked three questions at the outset of this dissertation: 1) How is genetic variation patterned in Central Asia?; 2) What, if any, geographic barriers have or continue to affect population interactions in Central Asia?; and 3) How has population history influenced the distribution of genetic variation that is seen in modern-day Central Asian populations? As a whole, Central Asia has largely been ignored in global studies of human genetic variation. Unfortunately, that means that currently there is a large geographic gap in the understanding of patterns of human genetic variation. As a result, my goal for this dissertation was not necessarily to support or refute any specific hypothesis, but rather to understand the patterning of genetic variation in Central Asia and to place it in a broader context. In order to address this objective, I focused my study on mtDNA. I do not suggest that this one source of data will provide definitive answers regarding the distribution of genetic variation in Central Asia; however, my intention was to examine genetic variation in Central Asia using a large, representative sample and a holistic perspective. I have framed my discussion around the three central questions raised in my Introduction and will discuss each now.

Genetic Variation in Central Asia

The big picture for this study was to examine genetic variation in Central Asia with the goal of including it in global models of human variation. At present, a

framework for understanding the genetic relationships among Central Asian populations is lacking. In particular, what is the population structure in this region? In examining this question it was clear that part of this study would have to be exploratory in nature. For the most part, rather than testing specific hypotheses I was more interested in identifying patterns of variation and proposing possible explanations for future study.

Population Structure in Central Asia

In order to assess population structure, I performed an AMOVA and calculated the genetic distances between all populations. The results of the AMOVA provide evidence that mtDNA sequence variation appears to be at least somewhat geographically structured, with 2.5% (p-value = 0.0000) of the genetic variation accounted for by differences between geographic regions; i.e., Caucasus North, Caucasus South, Central Asia, East Asia, East Europe, Near East, North Asia, North/Central Asia, North/East Asia, South Asia, and South/Central Asia. These results are not consistent with previous studies examining the same question. Zerjal et al. (2002) found a high degree of genetic structure in the Y-chromosome with close to 24% of variation occurring between populations; however, they were unable to identify a geographic or linguistic pattern to this variation. Segurel et al. (2008) analyzed X-linked markers and found significant between-group differences; however, they did not find any evidence of a correlation between geographic distance and genetic variation.

Within Central Asia, the Tajiks exhibited a unique pattern in several ways. First, they had high genetic distances relative to Kazakhstan, Kyrgyzstan, Turkmenistan, and

Uzbekistan. Additionally, in a few cases, populations outside of Central Asia were more similar to these four populations than Tajiks were. Other interesting patterns were observed with respect to the Tajiks. For example, the genetic distance between Kazakhs and Tajiks was greater than that between Kazakhs and Tuvinians. Tuvinians, like Kazakhs, are a Turkic-speaking group, while Tajiks are an Indo-European-speaking group. This shared language affiliation may be contributing to the short genetic distance detected between these two populations.

In addition, the genetic distance between Kyrgyz and Yakut was shorter than that between Kyrgyz and Tajiks. The Kyrgyz migrated south from the Upper Yenisei River region of Siberia following the conquest of Genghis Khan in the late 12th-century. The Yakut originated in the Lake Baikal region, which is located in southern Siberia and drains into the Yenisei River. The short genetic distance between the Kyrgyz and Yakut may be a reflection of the fact that they originated in the same geographic area and likely were regularly in contact with one another. Additionally, both the Kyrgyz and Yakut are Turkic-speaking groups so a shared linguistic background may also be contributing to their genetic similarity.

In terms of the degree of differences between groups, the Central Asian populations had short genetic distances among themselves and greater genetic distances with populations outside of Central Asia (Appendix B), which is consistent with geographic distance playing a role in the pattern of genetic variation in Central Asia. In order to more fully assess what may be contributing to the population structure identified

in this study, it is necessary to examine the haplotype and nucleotide diversity, mean number of pairwise differences within populations, and haplogroup frequencies.

High Genetic Diversity in Central Asia

The results of this dissertation support previous findings of high levels of genetic diversity in Central Asia (Calafell et al. 2000; Chaix et al. 2008; Comas et al. 1998; Comas et al. 2004). In general, the haplotype and nucleotide diversity as well as the mean number of pairwise differences within populations in Central Asia are high. This has been interpreted as the result of extensive admixture between East Asians and Europeans that occurred in Central Asia, framing this region as merely a genetic crossroads and melting pot rather than an innovator of molecular diversity (Calafell et al. 2000; Comas et al. 1998; Comas et al. 2004). However, high haplotype and nucleotide diversity as well as mean number of pairwise differences within populations can be the result of population age and size, not just admixture (Calafell et al. 2000; Comas et al. 1998; Quintana-Murci et al. 2004). Therefore, my results are consistent with an explanation of admixture, but they are also consistent with a scenario in which Central Asian populations have a deep antiquity and possibly even served as a source population for other parts of Eurasia (Andrews and Osborn 1926).

Genetic distances are also indicative of population structure in that they are a measure of the genetic similarity among populations. In this study, Central Asian populations generally presented the shortest genetic distances among themselves with a few exceptions. Both Kazakhstan and Tajikistan had the shortest genetic distances with

Bosnia; however, the most likely explanation for this is sample bias since the sample from Bosnia consisted of only five individuals. Because the sample size is included in the calculation of genetic distance, it can result in a falsely short genetic distance between populations (Nei 2002). Similarly, Uzbekistan had the shortest genetic distance with the Kalmyk sample, which is also quite small, only six individuals. However, the Kalmyk originated in Mongolia and only moved to their present location in SW Russia in the 17th century. Throughout history, Mongol groups have moved from this area into Central Asia and have contributed to the gene pool in this region. As such, it is very likely that Kalmyk and Uzbek share a history, which could also explain their genetic similarity. Kyrgyzstan had the shortest genetic distances with the Bargut and the Yakut. Both the Yakut and Kyrgyz originate from the same geographic area in Siberia and also share linguistic affiliation with one another. This provides a good explanation for their genetic similarity. The Bargut are a subgroup of the Mongol people and trace their origin to the Lake Baikal region of southern Siberia because the Kyrgyz originated in the same geographic area they likely had extensive contact, thus accounting for the short genetic distance between these two groups. Lastly, the Tajiks had the shortest genetic distance with the Dargin sample. There is no indication that Tajiks and Dargin share a history, overlapping geographic range, or language and so it is most probable that this result is due to sampling – the Dargin sample consists of only three individuals.

Given its geographic location, Central Asia would be expected to exhibit genetic distances with East Asia and East Europe that fall into the same range. In other words, it would be intermediate between East Asia and East Europe. However, the genetic

distances between the Central Asian and East Asian populations range from small to intermediate, while the genetic distances between Central Asia and Europe range from small to quite large (Appendix B). Specifically, Central Asian populations had small distances relative to the Bosnia, Moldova, and Tatar samples (East Europe) and the Bargut (East Asia) and Kalmyk (NE Asia) samples; and quite large distances relative to the East European Belarus, Chuvash, and Romania samples. Based on the ethnohistory of Central Asia, it is not surprising that small genetic distances were found between Central Asian populations and the Bargut, Kalmyk, and Tatar samples. The Bargut are a subgroup of the Mongol people and so would have had contact with the different peoples of Central Asia throughout their history, especially during and subsequent to the conquest of Central Asia by Genghis Khan. Similarly, the Kalmyk originated in Mongolia and as such are likely to have had extensive interactions with Central Asian populations. Additionally, during the latter part of WWII, Kalmyks were deported to Central Asia, which could also account for this small genetic distance. Lastly, the Tatars have Turkic ancestry just like several of the populations in Central Asia and so a short genetic distance is not remarkable. Also, beginning in the 18th and continuing into the 19th century, Tatars have immigrated to Central Asia for a variety of reasons including: a) as officers and soldiers, b) as part of the industrialization of Central Asia in the 1920s and 1930s, and c) as a part of the Soviet education program for Central Asian peoples. This history provides a reasonable explanation for the close genetic distances seen here.

The small genetic distances between Central Asian populations and Moldova and Bosnia may simply be the result of sampling bias as each of these samples were small,

four and five individuals, respectively. Bosniaks are a Slavic people and during the Soviet Empire many Slavic peoples immigrated to Central Asia; however, these were mostly Russians and Ukrainians. There does not seem to be any evidence that Bosniaks specifically immigrated to the region. Moldovans are closely related to Romanians and neither Romanians nor Moldovans seem to share any special history with populations from Central Asia. Additionally, the Romanian sample generally had a large genetic distance with Central Asian populations, and so I suspect that the small genetic distance between Moldova and Central Asian populations is the result of the sample size.

In addition to looking at large-scale east-west continental patterns, I also looked at Central Asia relative to the adjacent regions of North, South, and West Asia. Central Asian populations had small genetic distances with several populations from North Asia (Altaian Kazakh, Ket, Khamnigan, Mansi, Moldova, Negidal, Shor, Tuvinian, and Yakut) and the Caucasus and Near East regions (Adygei, Armenia, Iraq, and Kuwait). The small genetic distances with populations from North Asia and the Caucasus and Near East regions indicates that Central Asia cannot simply be considered intermediate between East Asia and Europe. There have been extensive historical interactions among populations from these regions and as such, it is not surprising to find small genetic distances. For example, Uzbekistan had short genetic distances with the Tatars, which is consistent with the movement of Volga Tatars into Central Asia as Russian officers, soldiers, tradesmen, and religious immigrants during the 19th century. Tatars also immigrated to Central Asia during the 1920s and 1930s as a part of industrialization, and then in the late 1940s and 1960s as part of the Soviet education program for Central Asia

peoples. As another example, the Kazakhs had a small genetic distance with the Mansi sample. The ancestors of the Mansi lived in the areas west of the Ural Mountains as well as in the south Ural steppe, located in northwestern Kazakhstan. Kazakhs have been nomadic herders throughout the steppe region for millennia and would have likely come into contact with the Mansi in this area of the Urals.

In general, Central Asian populations have a large number of different haplogroups (Appendix C), which provides further support for their high levels of genetic variation (Appendix D). The frequency of particular haplogroups provides insight on certain affinities. As discussed in the previous chapter, haplogroup H is the most frequent haplogroup in Central Asia, and is also a common haplogroup in Europe; although, it is thought to have originated in SW Asia (Achilli et al. 2004). There are several historical factors that likely contributed to the high frequency of haplogroup H in Central Asia. First, the existence of the Silk Road, an ancient network of trade routes that connected East to West and operated as the primary trade route between China, Central Asia, and Europe dating back to 100 BCE (Hiro 2009). This trade network may have contributed to increasing gene flow between Central Asians and Europeans traveling through the area. Second, haplogroup H is frequently found among Russians and because of the history of movements of Russians into Central Asia it is also likely that haplogroup H may have been introduced in that manner.

Other haplogroups with high frequency in the Central Asian sample are D4 and C, which are also common in East and Northeast Asia. Haplogroup D is thought to have arisen in Asia and D4 specifically is frequent in many populations from Northeast Asia

as well as China. Haplogroup C is frequent among Arctic populations (Comas et al. 2004; Volodko et al. 2008; Wen 2005). The frequencies of these two haplogroups in Central Asia are likely due to a variety of reasons: a) movement of Mongol tribes into Central Asia as a result of the conquest by Genghis Khan, b) interaction of populations through the Silk Road route, and c) geographic proximity to populations from the east, north, and northeast. In this study, several of the populations from North and North/Central Asia had high frequencies of haplogroup C. The Evenki, Khamnigan, and Yakut all originate from the Lake Baikal region. In particular, the Khamnigan come from the area where Genghis Khan was born and where he began to consolidate the Mongol tribes before he moved into Central Asia. Because Central Asian populations are known to have been influenced to a large extent by Mongol tribes, the high frequency of haplogroup C may have been introduced to Central Asia in this manner. Additionally, the Shor and Teleut from North/Central Asia also had high frequencies of haplogroup C. Both of these groups are Turkic-speakers and share a linguistic affiliation with the Turkic-speaking populations in Central Asia. Previous analyses using autosomal SNPs identified genetic structure that was shaped by linguistic affiliation (Martinez-Cruz et al. 2010). As discussed above, interactions as the result of the Silk Road may have brought both haplogroup C and D4 into Central Asia from the both East and North Asia. Lastly, Central Asia's geographic position in close proximity to populations from the east, north, and northeast may also have contributed to the high frequencies of haplogroups C and D4 in this region.

Additionally, two haplogroups, D4c and G2a, were also found in the current study at percentages of 1.36 and 2.41 in Central Asia. This is significant because 81.82% of D4c and 82.05% of G2a are found in Central Asia. Outside of Central Asia, haplogroup D4c was found in higher percentages among the Bargut (5%), Even (7.69%), Khamnigan (5%), and Ulchi (7.14%), while G2a was found in the Chinese (0.53%), Polish (5%), Szekely (0.56%), Tibetan (5%), Tuvinian (5.88%), and Ukrainian (5%) samples. Comas et al. (2004) explained this pattern as the result of these two haplogroups originating outside of Central Asia and their high frequency in this region can be explained by genetic drift during a founder event. However, an equally likely explanation is that these two haplogroups are representative of the first peopling of this region by early *Homo sapiens*. Molecular clock-mutation age calculations for these haplogroups were estimated as 25,000 ± 9,600 years for D4c and 29,500 ± 7,000 years for G2a. These two haplogroups may correspond with a Y-chromosome haplotype P(xR1a) that has been dated to 40,000 years, based on the formula $t = -N_e\ln(1 - V/N_e\mu)$ derived from a single step mutation model for a haploid population with constant size, and has a high frequency in Central Asia (Wells et al. 2001). Together these need to be investigated further to identify the probability of their geographic origin. In addition, ancient DNA analyses on mtDNA from this region would be useful in detecting the presence of these haplogroups in older populations.

Overall, most of the mtDNA haplogroups found in Central Asia belong to branches of haplogroups with an eastern Eurasian (A, B, C, D, F, G, M, and Y) or western Eurasian (HV, I, JT, N, and U) origin, with a small portion of Indian M lineages

(1.06%). The presence of such a high proportion of mtDNA sequences in Central Asia that originate elsewhere suggests that Central Asia has experienced high levels of gene flow.

To summarize, Central Asia contains four main lineage groups: 1) a group of lineages originating in western Eurasia; 2) a group of lineages originating in East Asia; 3) two locally expanded haplogroups (D4c and G2a); and 4) a small portion of sequences of Indian origin. The majority of lineages found have either an East Asian or a European origin. These are two non-overlapping mtDNA pools (Comas et al. 2004). This suggests that these two gene pools were already differentiated when they met in Central Asia, providing further support for the idea that the genetic diversity present in Central Asia has been influenced to a large extent by gene flow.

On the whole, the most likely explanation for the observed levels of genetic variation in Central Asia appears to be patterns of gene flow—low levels in some cases, high levels in others. Although these results are also consistent with patterns of diversity exhibited by large or old populations (Calafell et al. 2000), given what is known about the population history in this region, the most probable explanation is that admixture has played a significant role in the levels of mtDNA variation observed. A multitude of population movements and interactions within Central Asia have taken place relatively recently; as such, the admixture detected in this analysis most likely occurred within the last several thousand years.

The Role of Geographic Distance in Genetic Variation

The results of the AMOVA support the idea that geographic distance is playing a role in the distribution of genetic variation among the populations in this analysis. When all populations were treated as one group, the percentage of variation within populations was 96.32, while the percentage of variation among populations was 3.68 (Table 7.3). However, when the populations were grouped according to geographic region (defined in Chapter 5), the percentage of variation within populations fell to 93.46, while the percentage of variation among populations within groups was 4.04 and among groups 2.50 (Table 7.4). Thus, mtDNA diversity appears to be at least somewhat geographically structured, with 2.5% of the genetic variation accounted for by the differences between the geographic regions defined in this study.

I estimated an F_{ST} value (0.025) much lower than previous studies using other types of markers (Elhaik 2012; Latter 1980; Lewontin 1972; Livshits and Nei 1990; Nei and Roychoudhury 1982; Relethford 1994; Ryman et al. 1983; Stoneking 1993; Takahata 1993; Vigilant et al. 1991; Wilder et al. 2004), which range from 0.088 to 0.41. It is important to note that I have used a much finer scale for my geographic groupings. Although they do cover two continents, the geographic groupings are not as disparate as East Asia, Europe, and sub-Saharan Africa, for example. In addition, it can be difficult to compare the results of all of these studies, which have used different sample sizes, a wide variety of geographic groupings, and different types of genetic data. That being said, my results indicate that a small, but significant portion of human genetic variation

can be attributed to geographic distance as defined by the geographic regions used in my analysis.

The major geographic features that may serve as potential geographic barriers to population movements in Central Asia include the Caspian Sea and mountain ranges like the Altais, Himalayas, and Urals. Previous studies have not investigated whether these geographic features have been contributors to genetic discontinuity. In my study, populations on either side of these features did not have higher genetic distances. Therefore, although geographic distance is playing a role in the distribution of genetic variation, this result cannot be interpreted as indicative of any sort of geographic barriers. Instead, it appears more likely that a simple isolation by distance pattern of population structure whereby increased geographic distance has resulted in higher genetic distances between populations explains this result.

Haplogroup frequencies and genetic distances provide insight into this issue. The majority of haplogroups identified in Central Asia are believed to have either a European or East Asian origin. There are also a few haplogroups that originate from South Asia, namely India. This result indicates that Central Asia has experienced gene flow not only from the east and west, but also from the south. The PCA graph based on the haplogroup percentage matrix (Figure 4) shows an east to west clinal pattern, with populations from the west near the bottom, populations from the east near the top, and Central Asian populations in the middle. There are no sharp breaks like we would expect if there were some sort of geographic barrier disrupting population movements/interactions; on the

contrary, a clinal pattern is observed as would be expected based on an isolation by distance model.

If the genetic distances are taken into account (Appendix B), Central Asian populations demonstrate short genetic distances with several populations from the north including Altaian Kazakh, Ket, Mansi, Negidal, Tuvinian, and Yakut. This result is not an artifact of how Central Asia is defined in this study (Kazakhstan, Kyrgyzstan, Tajikistan, Turkmenistan, and Uzbekistan); even the broadest geographic definitions of Central Asia do not include the areas inhabited by these populations from the north, with the exception of the Altaian Kazakhs. The Altaian Kazakhs also share a history with the Kazakhs and this is the best explanation for the short genetic distances. Central Asian populations also demonstrate short genetic distances with populations from the south including Afghanistan, Armenia, Nepal, and Pakistan. Parts of Afghanistan and Pakistan have historically been included within Central Asia and so the short genetic distance between these populations may reflect a shared history and culture. On the other hand, both Armenia and Nepal are separated from Central Asia by significant geographic barriers (the Caspian Sea and the Himalayas, respectively) and yet still have small genetic distances with populations from Central Asia. Thus, providing evidence that population interactions have occurred with populations to the north and south of Central Asia, despite potential geographic barriers.

In summary, the observed pattern of genetic variation has been structured to a small, but significant extent by geographic distance as defined by the geographic regions used in my study. However, my results do not detect any sort of geographic barrier that

has affected or continues to affect population movements or interactions in Central Asia. Historical factors like the Silk Road and the wide variety of population movements into the area including Iranian, Turkic, Russian, Slavic, and other populations, are evident based on the population structure in this region.

Population History and Its Effect on Population Structure

Central Asia has a complex history of population interactions due to warfare, migration, trade, and a number of other factors. Until recently, Central Asia had not been studied much by Western scholars and its role in human history had been largely ignored. However, the brief history provided in chapter II serves to contextualize and interpret one of the important questions that the current research addresses: how has population history influenced the distribution of genetic variation that is observed in modern-day Central Asia? There are several specific questions that were mentioned during my historical review and I will address each here.

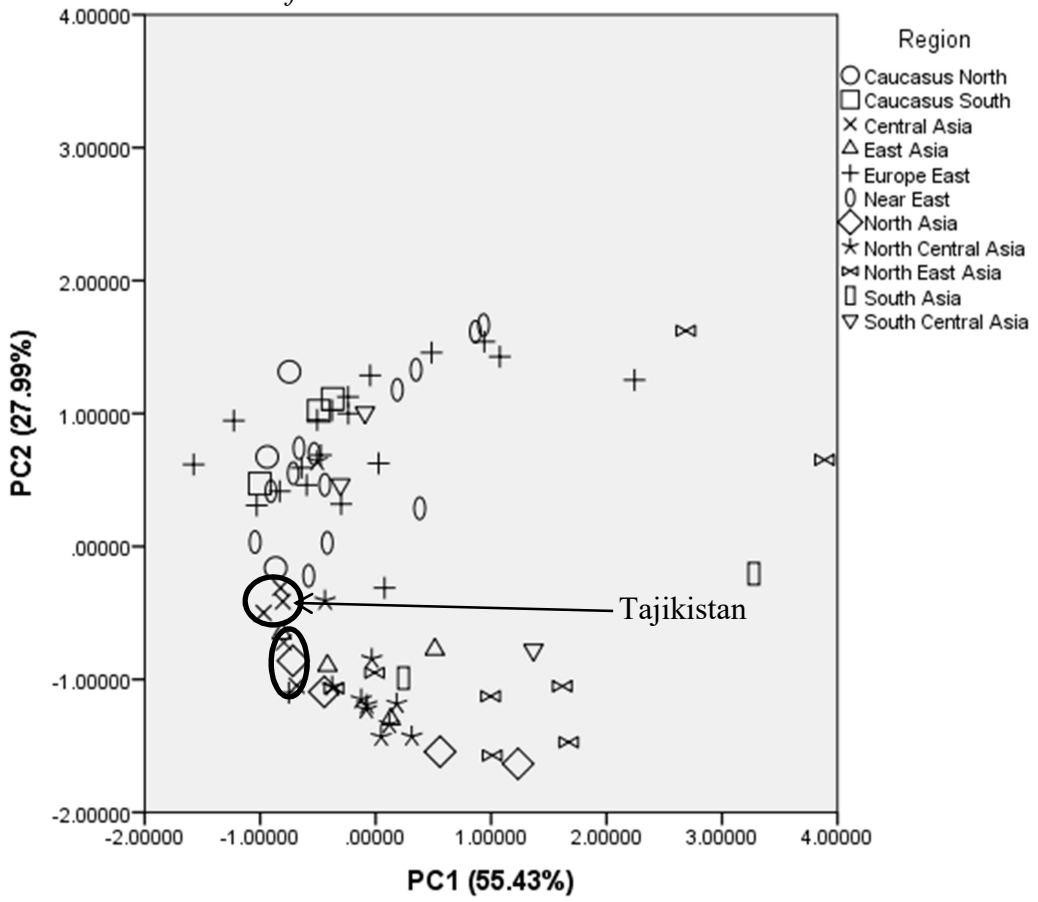
Q1: Did a replacement of Indo-European-speaking groups (Tajiks) by Turkic-speaking populations (Kazakhs, Kyrgyz, Turkmen, and Uzbeks) occur throughout Central Asia?

Today, Tajiks are considered the longest standing residents still living in Central Asia (Beckwith 2009; Subtelny 1994; Wheeler 1964). Archaeological evidence suggests that around 2000 BCE groups of Indo-Iranian tribes slowly moved southward from what is today Russia and emerged as the dominant ethnicity in Central Asia (Akiner 1997; Grousset 1970; Levi 2007). The populations that preceded them were either displaced or assimilated into Indo-Iranian tribal societies (Canfield 1991; Hiro 2009; Levi 2007).

These are the ancestors of the modern Tajiks, and they held a mostly uncontested position in these areas for about 2500 years (Bergne 2007; Levi 2007). However, beginning around 999 CE Turkic and later Mongol tribes began to move into the area and eventually Turkic language speakers became the dominant population of the region. As a result, the Indo-European-speaking Tajiks were either subsumed or relegated to the periphery of Central Asia (Akiner 1997; Bregel 1996; Levi 2007).

Based on historical records, it has been hypothesized that a replacement of Indo-European-speaking (Tajiks) groups by Turkic-speaking populations (Kazakhs, Kyrgyz, Turkmen, and Uzbeks) occurred throughout Central Asia. The genetic distances described in the previous chapter showed that Turkic-speaking populations had the highest genetic distances with Tajiks. Thus, the Turkic-speaking groups (Kazakhs, Kyrgyz, Turkmen, and Uzbek) are genetically more similar to one another than any are to the Tajiks. However, Figure 5 based on the PCA using the genetic distance matrix shows that Central Asian populations clustered together with Tajikistan, Turkmenistan, and Uzbekistan forming a tight cluster, while Kazakhstan and Kyrgyzstan were separated slightly. In fact, Tajikistan is in the middle between Uzbekistan and Turkmenistan. This result indicates that although the genetic distance between Tajiks and other Central Asian populations may be the highest within the region, these populations are still remarkably genetically similar when compared to populations outside of Central Asia.

FIGURE 5. *PCA from Genetic Distance Matrix with Central Asian Clusters*



In terms of haplogroup frequency, Tajikistan showed the lowest diversity. However, there was considerable overlap in the haplogroups represented in Tajikistan and the other Central Asian populations. I interpret this as evidence that rather than a replacement of Tajiks by Turkic-speaking populations, there is support for some degree of assimilation. Tajiks, Afghans, and Iranians all speak Persian languages and thus have a shared history with one another. The haplogroups present in Iran and Afghanistan are also present in Tajikistan, with one exception I. Because there is substantial overlap in

the haplogroups present in Tajikistan and other Central Asian populations, this is likely the result of admixture rather than replacement. One interesting finding was the lack of haplogroup D4c in Tajikistan. If this haplogroup is indeed representative of the first peopling of the region, it is somewhat surprising that it has not been identified among Tajiks, the population that has lived in Central Asia for the longest time frame. However, absence of D4c among the Tajik sample in the current study does not mean that it is not there or that it was not there at some point in time, but has been lost as the result of genetic drift or some other factor.

I predicted that Tajikistan would have lower levels of genetic diversity than other Central Asian populations reflecting a smaller population size as a result of replacement and/or relegation to a smaller geographic region. My results partially support this prediction; Tajiks had low haplotype and haplogroup diversity. However, they had the highest nucleotide diversity (along with Kazakhstan) and highest mean number of pairwise differences (Appendix C and Table 16). Previous analyses using 27 microsatellite markers found that Tajiks had high levels of diversity likely because they have been long-term residents in the area (Martinez-Cruz et al. 2010). The high nucleotide diversity and mean number of pairwise differences that I found in my analyses support this conclusion. I also hypothesized that levels of genetic similarity between Turkic-speaking populations should be higher than between these populations and Tajiks based on their shared history and language. I found that within Central Asia Tajikistan had the highest genetic distance with all other Central Asian populations. This

result indicates that Turkic-speaking groups are more genetically similar to one another than they are to Tajiks.

Taken all together, I did not find evidence of a complete replacement of Tajiks by Turkic-speaking groups. Although within Central Asia Turkic-speaking groups did have the highest genetic distances with Tajiks, the genetic distances were still low overall when compared with many of the other populations used in this analysis (Appendix B). The fact that Tajiks had low haplotype diversity can be explained as the result of their smaller population size, which would have occurred as the result of population pressures from Turkic and Mongol groups moving in and some Indo-European-speakers emigrating out of Central Asia. The overlap of haplogroups within Tajiks and other Central Asian populations (Appendix C) along with their position in both the PCA based on genetic distance (Figure 5) and that based on haplogroup frequencies (Figure 4) all support the idea that Tajiks were not replaced, but interacted extensively with other Central Asian populations.

Q2: Are Uzbeks and Kazakhs genetically more similar than either is with other Central Asian populations?

Kazakhs and Uzbeks did not separate into distinct ethnic groups until fairly recently; as such, I predicted a high degree of genetic similarity between these populations. I found that between Central Asian populations Kazakhstan had the shortest genetic distance with Uzbekistan (0.00506), but Uzbekistan actually had a shorter genetic distance with Turkmenistan (0.00261). The PCA based on the genetic distance matrix (Figure 4) showed that Kazakhstan and Uzbekistan were separated into two close,

but distinctive clusters among Central Asian populations. There is considerable overlap in the haplogroups represented in Kazakhs and Uzbeks and both have haplogroup H at the highest frequency; although, Kazakhs had an equally high frequency of D4 (Appendix C).

My results did not fully match my expectations given the history of Central Asia. However, it is not surprising that Uzbeks and Turkmen would be genetically very similar. Turkmenistan borders Uzbekistan to the south and the populations sampled may be geographically more proximate than the samples from Kazakhstan and Uzbekistan. Additionally, during the Soviet period Kazakhstan was separated from the remainder of Central Asia politically and economically. This may have also played a role in the genetic distances seen in the present study. Although Uzbekistan was more genetically similar to Turkmenistan, Uzbekistan and Kazakhstan still had a very low genetic distance (0.0056) demonstrating their close relationship.

Q3: Does the mtDNA variation present in Kazakhstan support the idea that they were the most "Russified" of the Central Asian states?

Kazakhstan was the first area to come under the control of the Russian Empire (Dunn and Dunn 1967; Gleason 1997; Levi 2007) and has been described as the most "Russified" of the Central Asian states. The process of Russification refers to the cultural assimilation of language and traditions. The results of my genetic distance analysis do not support the idea that Kazakhs were more open to marriage with Russians than other Central Asian populations. In fact, Tajikistan, Turkmenistan, and Uzbekistan all had a shorter genetic distance with Russia than Kazakhstan did. So despite the fact

that culturally Kazakhstan may have been the most assimilated, genetically they do not appear to have been more open to marriage with Russians than the other Central Asian populations, with the exception of Kyrgyzstan.

Summary

To summarize, the findings of my dissertation are consistent with previous research that has shown that Central Asian populations have high levels of genetic diversity (Calafell et al. 2000; Comas et al. 1998; Comas et al. 2004). This appears to be largely the result of admixture with surrounding populations; mostly, from the east and west, but also from the north and south. Based on the archaeological record, Central Asia has been occupied since at least the Lower Paleolithic (Glantz 2010; Ranov et al. 1995; Ranov and Davis 1979; Zerjal et al. 2002). Yet, the lack of basal mtDNA haplogroups in Central Asia and the high frequency of lineages belonging to external branches suggest that the mtDNA diversity found in this region is largely the result of admixture with previously differentiated populations. One important exception that bears further research is the identification of two haplogroups, D4c and G2a, that may be Central Asian specific. These haplogroups have been found in high frequencies in Central Asia and have been dated to 25,000 (D4c) and 29,000 (G2a). In general, my results contrast with those from Y-chromosome analyses, which suggest that the majority of Y lineages in Europe and Siberia came from the Middle East through Central Asia (Comas et al. 2004; Wells et al. 2001). This incongruity may be the result of different sex-based

patterns of migration in Central Asia. Data from the nuclear genome is necessary to clarify whether Central Asian populations may have an ancient origin.

In the process of examining the population structure and history of Central Asia, I found evidence that mtDNA diversity is geographically structured. I identified a small, but significant percentage of mtDNA variation that can be attributed to geographic distance as defined by geographic region. It is important to keep in mind that many factors may result in a misleading picture of population structure including balancing selection, the presence of selective clines, and variation in levels of gene flow (Muirhead 2001; Relethford 2004; Wright 1939). I used the mtDNA control region for this study and thus levels of gene flow will not affect the population structure detected in this study. The control region of mtDNA is considered to be a non-coding region of DNA and is the most polymorphic region of the human mitochondrial genome, making it useful for population level analyses (Stoneking 2000). In general, because it is non-coding most of the control region has not been affected by selection; however, an RNA transcript in this region has been shown to be under selective pressure (Pereira et al. 2008). Therefore, balancing selection or the presence of selective clines may have an influence on the population structure that I have identified.

Also, efforts to tease apart the effects of population history and structure may be confounded by the fact that a similarity between gene frequencies may reflect common ancestry or evolutionary forces, historical events, and/or mate exchange (Harpending and Jenkins 1973; Templeton et al. 1995). In addition, different patterns of genetic variation may result from uniparentally inherited versus diploid loci. This is of particular

relevance to the present study, which utilizes mtDNA. Any interpretation of the genetic variation based on mtDNA must take into account that mtDNA is maternally inherited and, as such, may show patterns of variation that are based on sex-specific migration patterns (Chaix et al. 2007; Segurel et al. 2008). These confounding factors must be mentioned when considering the results of this study.

As to the question of what this geographic structure means, I was unable to fully answer the question of whether geographic barriers have affected gene flow within Central Asia. The AMOVA that I used to address this question was able to identify the presence of geographic structure, but I was not able to conclusively determine whether this may simply be caused by a correlation between genetic distance and geographic distance as has been demonstrated in a number of other population studies (Relethford 2004). That being said, the presence of East Asian, European, and South Asian mtDNA haplogroups in Central Asia combined with the close genetic distances found between Central Asia and East Asia, East Europe, the Near East, North Asia, and the Caucasus region all suggest that there have not been any geographic impediments to population movements and interactions in this region.

Lastly, the complex history of Central Asia can be evidenced in the patterning of genetic variation in this region. Central Asian populations are genetically similar to one another including both Indo-European-speaking groups as well as Turkic-speaking populations. The presence of haplogroups from Europe, East Asia, and North and South Asia are evidence of the complex population movements that have taken place throughout history. This includes movements that have occurred thousands of years ago,

like the conquest of Central Asia by Genghis Khan and the subsequent interactions of Mongol groups with the residents of Central Asia, and those that have happened more recently, such as the movement of Volga Tatars into Central Asia during the 18th, 19th, and 20th centuries. The genetic structure of mtDNA in Central Asia has been influenced to a large extent by the population history in this region.

CHAPTER IX

CONCLUSIONS

Central Asia is an area with a diverse history; a history that has been molded by cultural and linguistic changes brought about by trade, internal and external migrations, and warfare (Comas et al. 1998; Comas et al. 2004). Partly because of the Silk Road, it is an area that is often seen as a crossroads between East and West. Despite its centralized location and rich history, many have thought of Central Asia as lacking a unique history (Bowles 1977; Comas et al. 2004; Sellier and Sellier 1993). Yet, it is an area that has played a critical, though poorly understood, role in human history (Calafell et al. 2000; Comas et al. 1998).

Morphological and genetic studies of Central Asia have largely considered Central Asian populations to be the result of admixture between differentiated populations from Europe and East Asia (Bowles 1977; Calafell et al. 2000; Comas et al. 1998; Comas et al. 2004; Ginzburg 1968a; Ginzburg 1968b). I believe that these findings have contributed to the fallacy that Central Asia is an area without a unique history. My dissertation has used a holistic perspective to examine genetic variation in Central Asia, resulting in a more detailed understanding of the genetic relationships among Central Asian populations as well as the relationship of Central Asia to neighboring regions.

In so doing, I have answered three questions that were raised in my Introduction. First, I inquired as to the patterning of genetic variation in Central Asia. Based on the AMOVA, I was able to identify a geographic pattern to the mtDNA variation in Central

Asia and the surrounding areas. This result was further supported by the calculation of genetic distances between populations, which showed that generally Central Asian populations had short genetic distances among themselves and larger genetic distances with other populations. I also found that based on the haplotype diversity, nucleotide, diversity, and mean number of pairwise differences within populations Central Asian populations exhibit a high degree of genetic diversity. Additionally, Central Asian populations had a large number of different haplogroups providing further support for their high levels of genetic variation. The majority of haplogroups identified within Central Asia have either an East or West Eurasian origin, but there was also a small percentage of haplogroups found that originate from India. There were also two haplogroups identified, D4c and G2a, that may have their origins in Central Asia as they are found at high frequency in populations from this region. In addition, my results showed that Central Asia had short genetic distances with populations from East Europe and East Asia as well as populations from the Near East, Caucasus region, and northern Asia. These results indicate that genetic variation in Central Asia has been shaped to a large extent by admixture with multiple populations from neighboring regions. Most of this genetic variation is the result of relatively recent population movements; however, the presence of haplogroups D4c and G2a may date back to the first peopling of this region.

The use of mtDNA as the data source for this study did have limitations. It must be stressed that because my study uses mtDNA sequences only the female lineages are taken into account. This is of particular relevance to the patterning of genetic variation in

Central Asia because historically Central Asia has been subjected to invasions by nomadic peoples and it is likely that processes like invasions would have been carried out by male warriors. This is something that is important to keep in mind when interpreting the relationship of Central Asian populations with populations like the Mongolians or Turks, for example. My analyses did not identify any particularly close genetic relationship between Central Asian populations and the samples from Turkey or Mongolia. This should not be interpreted as evidence that they do not share any genetic similarities; rather it is likely that it is not being detected in the mtDNA analyses.

The second question posed in the Introduction was whether there had been any geographic barriers to gene flow in Central Asia. I found that a small, but significant portion of the mtDNA variation in Central Asia can be accounted for by geographic distance as defined by geographic region. Although there are several geographic barriers that have the potential to disrupt population movements into Central Asia (e.g., Altai Mountains, Caspian Sea, Himalayas), I did not find any evidence that this was the case. The presence of haplogroups in Central Asia that originate in East and West Eurasia as well as South Asia indicates that there has not been a disruption in population movements from the east, west, or south. Additionally, Central Asian populations demonstrate short genetic distances with several populations from the north including the Altaian Kazakhs and populations from the south including Armenia and Nepal. These populations are separated from Central Asia by significant geographic barriers and yet still have small genetic distances with populations from this region.

My ability to answer this question was somewhat limited because AMOVA can only answer the question of whether the grouping applied is significant. It cannot determine what may have caused that grouping or why it is significant. However, by comparing my results to those from previous analyses and also examining the genetic distances between populations I am able to draw conclusions about the presence of geographic barriers that may have limited population interactions in Central Asia. My results do not detect any sort of geographic barrier that has or continues to affect population movements in Central Asia. Rather the geographic structure that I identified is most consistent with an increase in genetic distance corresponding with increased geographic distance.

The last question presented in my Introduction is where the use of a holistic perspective really comes into play: how has population history influenced the distribution of genetic variation in modern-day Central Asian populations? There were several specific questions that were included within this broader issue including the relationship of Tajiks and Turkic-speaking groups in Central Asia, the genetic similarity of Uzbeks and Kazakhs, and the degree of admixture between Kazakhs and Russians. My results indicate that rather than a replacement of Tajiks by Turkic-speaking groups, there is evidence that these groups interacted extensively. In terms of the genetic relationship between Uzbeks and Kazakhs, I found that though these two groups share a small genetic distance, Uzbeks share more genetic similarities with Turkmen. I believe that this is because of the geographic proximity of Turkmenistan and Uzbekistan as well as the fact that during the Soviet period Kazakhstan was separated politically and

economically from the rest of Central Asia. Lastly, I did not find evidence that the cultural Russification of Kazakhstan resulted in an increase in the genetic similarity between Russians and Kazakhs. In fact, with the exception of Kyrgyzstan, all other Central Asian populations were more genetically similar to Russians that the Kazakhs were.

In summary, I conclude that Central Asian populations exhibit a high degree of genetic variation. I suggest that this genetic variation has been shaped to a large extent by admixture with populations mainly from East and West Eurasia, but also indigenous groups from North Asia as well as South Asia. To put it simply, Central Asia, with its unique history and central location, has been a place of contact for populations throughout Eurasia. My results should not be taken to imply that Central Asian populations can simply be viewed as intermediate between Europe and East Asia. This is not the case, and in fact, such an observation obscures the complex forces that have shaped the genetic variation in Central Asia.

The idea that the genetic diversity in Central Asia is intermediate to Europe and Asia suggests that this region does not have its own history and that it has not contributed to either the earliest movements of *Homo sapiens* or to human history in general. This is just not the case. Central Asia has been occupied since at least the Lower Paleolithic and the people there did not simply disappear or fail to contribute to human genetic variation. The presence of two possible Central Asian specific haplogroups must be investigated as these two haplogroups may provide evidence of the first peopling of

this region. They also have the potential to answer questions about the pattern of dispersal of early *Homo sapiens*.

I also found that a small, but significant portion of the variation in Central Asia can be accounted for by geographic distance as defined by geographic region. I do not propose that this is because of any geographic barriers to gene flow; instead, I suggest that this geographic structuring is most consistent with an increase in genetic distance corresponding with increased geographic distance.

As for the effects of population history on population structure, my results make it clear that in order to understand the population structure of Central Asia, population history must be taken into account. The history of population interactions within Central Asia has influenced the distribution of genetic variation in this region to a great extent. This is evident in the high levels of genetic diversity present within Central Asian populations as a whole as well as their genetic similarities to populations from East and West Eurasia as well as North and South Asia.

In conclusion, this dissertation has been a step in the right direction and has begun the process of placing Central Asia in its proper position in global models of human genetic variation. It is now possible to begin to build a truly representative framework of human variation that can be used to test hypotheses regarding modern human origins, Middle and Late Pleistocene hominin interactions, and the geographic distribution of Neandertal populations. The remaining challenge is to step away from simple explanations of genetic variation that fall back on the idea that Central Asian

populations are intermediate and to really attempt to understand not only the influence of historical events on Central Asian genetic variation, but also evolutionary factors.

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APPENDIX A

TABLE OF MTDNA SEQUENCES AND HAPLOGROUPS

Population	**GenBank**	**Reference**	**Haplogroup (HG)**
Adygei	AY882398	Achilli et al. (2005)	U5a1
Adygei	AY882396	Achilli et al. (2005)	U1a
Adygei	AY882388	Achilli et al. (2005)	U4b
Adygei	AY882384	Achilli et al. (2005)	U3b
Afghanistan	GU069335	Irwin et al. (2010)	H6
Afghanistan	GU069336	Irwin et al. (2010)	M7b2
Afghanistan	GU069337	Irwin et al. (2010)	M7b2
Afghanistan	GU069338	Irwin et al. (2010)	U2e1
Afghanistan	GU069339	Irwin et al. (2010)	H1+16189
Afghanistan	GU069340	Irwin et al. (2010)	M3a1+204
Afghanistan	GU069341	Irwin et al. (2010)	H1u2
Afghanistan	GU069342	Irwin et al. (2010)	G3a1
Afghanistan	GU069343	Irwin et al. (2010)	T2d1
Afghanistan	GU069344	Irwin et al. (2010)	CZ
Afghanistan	GU069345	Irwin et al. (2010)	U4
Afghanistan	GU069346	Irwin et al. (2010)	D4j3
Afghanistan	GU069347	Irwin et al. (2010)	T2d1
Afghanistan	GU069348	Irwin et al. (2010)	K1a11
Afghanistan	GU069349	Irwin et al. (2010)	D4k
Afghanistan	GU069350	Irwin et al. (2010)	C4a1a+195
Afghanistan	GU069351	Irwin et al. (2010)	T2d1
Afghanistan	GU069352	Irwin et al. (2010)	K1a4c
Afghanistan	GU069353	Irwin et al. (2010)	N1b1
Afghanistan	GU069354	Irwin et al. (2010)	U7a
Afghanistan	GU069355	Irwin et al. (2010)	U7a
Afghanistan	GU069356	Irwin et al. (2010)	H1+16189
Afghanistan	GU069357	Irwin et al. (2010)	K1a4c
Afghanistan	GU069358	Irwin et al. (2010)	K1a4c
Afghanistan	GU069359	Irwin et al. (2010)	K1a11
Afghanistan	GU069360	Irwin et al. (2010)	K1a4c
Afghanistan	GU069361	Irwin et al. (2010)	K1a11

Population	GenBank	Reference	Haplogroup (HG)
Afghanistan	GU069362	Irwin et al. (2010)	U7a2a
Afghanistan	GU069363	Irwin et al. (2010)	K1a11
Afghanistan	GU069364	Irwin et al. (2010)	K1a11
Afghanistan	GU069365	Irwin et al. (2010)	CZ
Afghanistan	GU069366	Irwin et al. (2010)	U3a
Afghanistan	GU069367	Irwin et al. (2010)	U1a
Afghanistan	GU069368	Irwin et al. (2010)	U7a
Afghanistan	GU069369	Irwin et al. (2010)	K1a11
Afghanistan	GU069370	Irwin et al. (2010)	K1a11
Afghanistan	GU069371	Irwin et al. (2010)	K1a11
Afghanistan	GU069372	Irwin et al. (2010)	K1a4c
Afghanistan	GU069373	Irwin et al. (2010)	K1a11
Afghanistan	GU069374	Irwin et al. (2010)	H13a1a2a
Afghanistan	GU069375	Irwin et al. (2010)	K1a11
Afghanistan	GU069376	Irwin et al. (2010)	M3
Afghanistan	GU069377	Irwin et al. (2010)	H6
Afghanistan	GU069378	Irwin et al. (2010)	H13a1a2a
Afghanistan	GU069379	Irwin et al. (2010)	K1a11
Afghanistan	GU069380	Irwin et al. (2010)	N3
Afghanistan	GU069381	Irwin et al. (2010)	K1a11
Afghanistan	GU069382	Irwin et al. (2010)	H13a1a2a
Afghanistan	GU069383	Irwin et al. (2010)	K1a4c
Afghanistan	GU069384	Irwin et al. (2010)	K1a11
Afghanistan	GU069385	Irwin et al. (2010)	U2e1
Afghanistan	GU069386	Irwin et al. (2010)	U2e1
Afghanistan	GU069387	Irwin et al. (2010)	K1a11
Afghanistan	GU069388	Irwin et al. (2010)	M33a1b
Afghanistan	GU069389	Irwin et al. (2010)	A11
Afghanistan	GU069390	Irwin et al. (2010)	K1a11
Afghanistan	GU069391	Irwin et al. (2010)	H13a1a2a
Afghanistan	GU069392	Irwin et al. (2010)	H13a1a2a
Afghanistan	GU069393	Irwin et al. (2010)	H13a1a2a
Afghanistan	GU069394	Irwin et al. (2010)	U1a
Afghanistan	GU069395	Irwin et al. (2010)	H2a2a
Afghanistan	GU069396	Irwin et al. (2010)	K1a11
Afghanistan	GU069397	Irwin et al. (2010)	H13a1a2a

Population	GenBank	Reference	Haplogroup (HG)
Afghanistan	GU069398	Irwin et al. (2010)	J1d
Afghanistan	GU069399	Irwin et al. (2010)	H13a1a2a
Afghanistan	GU069400	Irwin et al. (2010)	H2a2a
Afghanistan	GU069401	Irwin et al. (2010)	H2a2a
Afghanistan	GU069402	Irwin et al. (2010)	U8c
Afghanistan	GU069403	Irwin et al. (2010)	U8c
Afghanistan	GU069404	Irwin et al. (2010)	T2d1
Afghanistan	GU069405	Irwin et al. (2010)	U4
Afghanistan	GU069406	Irwin et al. (2010)	M30+16234
Afghanistan	GU069407	Irwin et al. (2010)	U4
Afghanistan	GU069408	Irwin et al. (2010)	C4a1a+195
Afghanistan	GU069409	Irwin et al. (2010)	M3
Afghanistan	GU069410	Irwin et al. (2010)	U4
Afghanistan	GU069411	Irwin et al. (2010)	U4
Afghanistan	GU069412	Irwin et al. (2010)	T
Afghanistan	GU069413	Irwin et al. (2010)	U1a1d
Afghanistan	GU069414	Irwin et al. (2010)	H5a4
Afghanistan	GU069415	Irwin et al. (2010)	G2c
Afghanistan	GU069416	Irwin et al. (2010)	HV1
Afghanistan	GU069417	Irwin et al. (2010)	H2a2a
Afghanistan	GU069418	Irwin et al. (2010)	K1a11
Afghanistan	GU069419	Irwin et al. (2010)	U2e1
Afghanistan	GU069420	Irwin et al. (2010)	H13a1a2a
Afghanistan	GU069421	Irwin et al. (2010)	B4c1a2a
Afghanistan	GU069422	Irwin et al. (2010)	U3a
Afghanistan	GU069423	Irwin et al. (2010)	U3a
Afghanistan	GU069424	Irwin et al. (2010)	U1a
Afghanistan	GU069425	Irwin et al. (2010)	K1a11
Afghanistan	GU069426	Irwin et al. (2010)	K1a11
Afghanistan	JF742450	Irwin et al. (2010)	U3a
Afghanistan	GU069428	Irwin et al. (2010)	A11
Afghanistan	GU069429	Irwin et al. (2010)	A11
Afghanistan	GU069430	Irwin et al. (2010)	H3h7
Afghanistan	GU069431	Irwin et al. (2010)	M30b
Afghanistan	GU069432	Irwin et al. (2010)	H2a2a
Albania	JQ797817	Pala et al. (2012)	J1c2a5

Population	GenBank	Reference	Haplogroup (HG)
Albania	JQ797974	Pala et al. (2012)	J2b2
Albania	KC867126	Kushniarevich et al. (2013)	N3a
Albania	EF660979	Gasparre et al. (2007)	V1a
Albania	JQ706027	Behar et al. (2012)	K1a8b
Altaian Kazakh	JN857054	Derenko et al. (2012)	M9a1b2
Altaian Kazakh	FJ951600	Derenko et al. (2010)	D4p
Altaian Kazakh	KJ856680	Derenko et al. (2014)	Hv12b1
Altaian Kazakh	KJ856705	Derenko et al. (2014)	U2e1i
Altaian Kazakh	KJ856706	Derenko et al. (2014)	H*
Altaian Kazakh	KJ856709	Derenko et al. (2014)	H15b
Altaian Kazakh	KJ856713	Derenko et al. (2014)	H11a2a2
Altaian Kazakh	KJ856717	Derenko et al. (2014)	H2a1a*
Altaian Kazakh	KJ856718	Derenko et al. (2014)	U4a2a*
Altaian Kazakh	KJ856726	Derenko et al. (2014)	H2b
Altaian Kazakh	KJ856727	Derenko et al. (2014)	U4a2a*
Altaian Kazakh	KJ856728	Derenko et al. (2014)	H1*
Altaian Kazakh	KJ856732	Derenko et al. (2014)	H1*
Armenia	JQ797846	Pala et al. (2012)	J1c7
Armenia	HM852756	Schoenberg et al. (2011)	X2f1
Armenia	HM852757	Schoenberg et al. (2011)	H13a2b1
Armenia	HM852758	Schoenberg et al. (2011)	X2e1b
Armenia	HM852759	Schoenberg et al. (2011)	U8b1a1
Armenia	HM852760	Schoenberg et al. (2011)	H
Armenia	HM852761	Schoenberg et al. (2011)	HV1a1
Armenia	HM852762	Schoenberg et al. (2011)	K1a
Armenia	HM852763	Schoenberg et al. (2011)	K1b2a
Armenia	HM852764	Schoenberg et al. (2011)	X2c
Armenia	HM852765	Schoenberg et al. (2011)	J1b9
Armenia	HM852766	Schoenberg et al. (2011)	T2+16189
Armenia	HM852767	Schoenberg et al. (2011)	H7b1
Armenia	HM852768	Schoenberg et al. (2011)	N1b1a2
Armenia	HM852769	Schoenberg et al. (2011)	U4a2a
Armenia	HM852770	Schoenberg et al. (2011)	U3b2
Armenia	HM852771	Schoenberg et al. (2011)	H2a3
Armenia	HM852772	Schoenberg et al. (2011)	U1b2
Armenia	HM852773	Schoenberg et al. (2011)	U3b2c

Population	GenBank	Reference	Haplogroup (HG)
Armenia	HM852774	Schoenberg et al. (2011)	J1c2
Altaian Kizhi	JN857015	Derenko et al. (2012)	B5b3
Altaian Kizhi	JN857014	Derenko et al. (2012)	B4b1a3a1a
Altaian Kizhi	JN857013	Derenko et al. (2012)	M10a1a2a
Altaian Kizhi	JN857012	Derenko et al. (2012)	R11b1
Altaian Kizhi	JN857011	Derenko et al. (2012)	B4b1a3a1
Altaian Kizhi	JN857010	Derenko et al. (2012)	M11b2
Altaian Kizhi	FJ951439	Derenko et al. (2010)	C5a1
Altaian Kizhi	FJ951440	Derenko et al. (2010)	C5*
Altaian Kizhi	FJ951441	Derenko et al. (2010)	C5b1a
Altaian Kizhi	FJ951442	Derenko et al. (2010)	C4a1b2
Altaian Kizhi	FJ951443	Derenko et al. (2010)	C4a1a
Altaian Kizhi	FJ951444	Derenko et al. (2010)	C4a1b2
Altaian Kizhi	FJ951445	Derenko et al. (2010)	C4b*
Altaian Kizhi	FJ951446	Derenko et al. (2010)	D4b1a2
Altaian Kizhi	FJ951447	Derenko et al. (2010)	C4b3
Altaian Kizhi	FJ951448	Derenko et al. (2010)	D4r
Altaian Kizhi	FJ951449	Derenko et al. (2010)	C4a2a1
Altaian Kizhi	FJ951450	Derenko et al. (2010)	D4e4
Altaian Kizhi	FJ951451	Derenko et al. (2010)	C4b6
Altaian Kizhi	EF153772	Derenko et al. (2007)	X2e
Azerbaijan	JQ797874	Pala et al. (2012)	J1c
Azerbaijan	JQ797975	Pala et al. (2012)	T1
Azerbaijan	JQ798009	Pala et al. (2012)	T1a1b
Azerbaijan	JQ798035	Pala et al. (2012)	T1a4b
Azerbaijan	JQ798057	Pala et al. (2012)	T2a1b2
Azerbaijan	JQ798133	Pala et al. (2012)	T2
Azerbaijan	HM852786	Schoenberg et al. (2011)	R1a1
Azerbaijan	HM852787	Schoenberg et al. (2011)	H
Azerbaijan	HM852788	Schoenberg et al. (2011)	U7a4a1a
Azerbaijan	HM852789	Schoenberg et al. (2011)	U1a2
Azerbaijan	HM852790	Schoenberg et al. (2011)	U1a1
Azerbaijan	HM852791	Schoenberg et al. (2011)	U7a4a1
Azerbaijan	HM852792	Schoenberg et al. (2011)	HV9c
Azerbaijan	HM852793	Schoenberg et al. (2011)	J1c15a1
Azerbaijan	HM852794	Schoenberg et al. (2011)	F1b1+@152

Population	GenBank	Reference	Haplogroup (HG)
Azerbaijan	HM852795	Schoenberg et al. (2011)	H
Azerbaijan	HM852796	Schoenberg et al. (2011)	T2h
Azerbaijan	HM852797	Schoenberg et al. (2011)	U3c
Azerbaijan	HM852798	Schoenberg et al. (2011)	T1a1b1
Azerbaijan	HM852799	Schoenberg et al. (2011)	X2
Bargut	JN857034	Derenko et al. (2012)	F2d
Bargut	JN857033	Derenko et al. (2012)	N9a2*
Bargut	JN857032	Derenko et al. (2012)	R9c2
Bargut	JN857031	Derenko et al. (2012)	B4c1a2a
Bargut	JN857030	Derenko et al. (2012)	N9a2f
Bargut	JN857029	Derenko et al. (2012)	B4d1
Bargut	JN857028	Derenko et al. (2012)	M13a1b
Bargut	FJ951509	Derenko et al. (2010)	D4m1
Bargut	FJ951510	Derenko et al. (2010)	D4q
Bargut	FJ951511	Derenko et al. (2010)	D4b1a2
Bargut	FJ951512	Derenko et al. (2010)	C4b1
Bargut	FJ951513	Derenko et al. (2010)	D5a2b
Bargut	FJ951514	Derenko et al. (2010)	D4b2c
Bargut	FJ951515	Derenko et al. (2010)	C5a1
Bargut	FJ951516	Derenko et al. (2010)	D4j5
Bargut	FJ951517	Derenko et al. (2010)	D4a1d
Bargut	FJ951518	Derenko et al. (2010)	C4a1a
Bargut	FJ951519	Derenko et al. (2010)	D4h4
Bargut	FJ951520	Derenko et al. (2010)	D2b2
Bargut	FJ951521	Derenko et al. (2010)	D4c2b
Belarus	JQ797855	Pala et al. (2012)	J1c7a1
Belarus	JQ797856	Pala et al. (2012)	J1c7a1a
Belarus	JQ797857	Pala et al. (2012)	J1c7a1a
Belarus	EU545465.2	Malyarchuk et al. (2008a)	U4c
Belarus	EU545464.2	Malyarchuk et al. (2008a)	U4a2
Belarus	EU545430.2	Malyarchuk et al. (2008a)	U4a2
Belarus	EU545415.2	Malyarchuk et al. (2008a)	U4b
Belarus	GU296578	Malyarchuk et al. (2010a)	U5a2b1
Belarus	GU296579	Malyarchuk et al. (2010a)	U5b1b1a
Belarus	GU296580	Malyarchuk et al. (2010a)	U5a2a
Belarus	GU296581	Malyarchuk et al. (2010a)	U5a1a1a1

Population	GenBank	Reference	Haplogroup (HG)
Belarus	GU296582	Malyarchuk et al. (2010a)	U5b1b'c
Belarus	GU296583	Malyarchuk et al. (2010a)	U5a1a1a1
Belarus	GU296648	Malyarchuk et al. (2010a)	U5a2e
Belarus	GU296649	Malyarchuk et al. (2010a)	U5a1b1b
Belarus	GU296650	Malyarchuk et al. (2010a)	U5a2a
Belarus	GU296651	Malyarchuk et al. (2010a)	U5a2b1
Belarus	GU296652	Malyarchuk et al. (2010a)	U5a1a1a1
Belarus	GU296653	Malyarchuk et al. (2010a)	U5a2b1
Belarus	GU296654	Malyarchuk et al. (2010a)	U5b1b1a
Bosnia	JQ797852	Pala et al. (2012)	J1c7
Bosnia	KP340174	DeFanti et al. (2015)	HV4a1
Bosnia	KT901290	direct submission	H1b2
Bosnia	GQ129145	Pala et al. (2009)	U5b3
Bosnia	KM103655	Kovacevic et al. (2014)	K1a13a
Bulgaria	JQ245742	Fernandes et al. (2012)	N1b1
Bulgaria	JQ245743	Fernandes et al. (2012)	W3
Bulgaria	JQ245807	Fernandes et al. (2012)	I5a1
Bulgaria	KP407069	Gandini et al. (unpub)	R0a2r
Bulgaria	KJ600772	direct submission	T1a1I
Bulgaria	KX021310	direct submission	H4a1a1a
Bulgaria	KU961659	direct submission	H7b1
Bulgaria	KX017522	direct submission	H56a1
Bulgaria	KU754494	direct submission	H44b
Bulgaria	KT884832	direct submission	H14a2
Bulgaria	KT828339	direct submission	H2a2a1
Bulgaria	KT799551	direct submission	H44b
Bulgaria	KT778765	direct submission	H27
Bulgaria	KT779554	direct submission	H7c1
Bulgaria	KT634229	direct submission	K1a4
Bulgaria	KR137642	direct submission	T1a1I
Bulgaria	KP969065	direct submission	H1c7
Bulgaria	KP860337	direct submission	U4a1a1
Bulgaria	KP797881	direct submission	T1a
Bulgaria	KM013847	direct submission	T2f2
Buryat	JN857027	Derenko et al. (2012)	N9a7
Buryat	JN857026	Derenko et al. (2012)	B4b1a3a1a
Buryat	JN857025	Derenko et al. (2012)	B4c1a2
Buryat	JN857024	Derenko et al. (2012)	M11a

Population	GenBank	Reference	Haplogroup (HG)
Buryat	JN857023	Derenko et al. (2012)	N9a3
Buryat	JN857022	Derenko et al. (2012)	B4b1a3a
Buryat	JN857021	Derenko et al. (2012)	B4c1a2
Buryat	JN857020	Derenko et al. (2012)	M13a1b
Buryat	JN857019	Derenko et al. (2012)	B4c1a2
Buryat	JN857018	Derenko et al. (2012)	M9a1a1c1b1a1
Buryat	JN857017	Derenko et al. (2012)	B4i
Buryat	JN857016	Derenko et al. (2012)	B5b2b
Buryat	FJ951456	Derenko et al. (2010)	D4j3
Buryat	FJ951457	Derenko et al. (2010)	C5a2*
Buryat	FJ951458	Derenko et al. (2010)	D4j*
Buryat	FJ951459	Derenko et al. (2010)	C4a1a
Buryat	FJ951460	Derenko et al. (2010)	C4b5
Buryat	FJ951461	Derenko et al. (2010)	D4m1
Buryat	FJ951462	Derenko et al. (2010)	C4a1b1
Buryat	FJ951463	Derenko et al. (2010)	C4a1b2
China	FJ026015	Irwin et al. (2009)	F1a1a
China	FJ026016	Irwin et al. (2009)	F1a
China	FJ026017	Irwin et al. (2009)	C
China	FJ026018	Irwin et al. (2009)	D5b4
China	FJ026019	Irwin et al. (2009)	C4b8a
China	FJ026020	Irwin et al. (2009)	D4a3b2
China	FJ026021	Irwin et al. (2009)	D5a2a1+@16172
China	FJ026022	Irwin et al. (2009)	B4c1a1a1a
China	FJ026023	Irwin et al. (2009)	D4b2b
China	FJ026024	Irwin et al. (2009)	B6a1
China	FJ026025	Irwin et al. (2009)	F2b1
China	FJ026026	Irwin et al. (2009)	D4a3b2
China	FJ026027	Irwin et al. (2009)	A15
China	FJ026028	Irwin et al. (2009)	F1a1
China	FJ026029	Irwin et al. (2009)	B6a1
China	FJ026030	Irwin et al. (2009)	Z+152
China	FJ026031	Irwin et al. (2009)	B2o1a
China	FJ026032	Irwin et al. (2009)	M7b1a1a1
China	FJ026033	Irwin et al. (2009)	A6b
China	FJ026034	Irwin et al. (2009)	F1a1d

Population	GenBank	Reference	Haplogroup (HG)
China	FJ026035	Irwin et al. (2009)	D5a2a1b1
China	FJ026036	Irwin et al. (2009)	B4e
China	FJ026037	Irwin et al. (2009)	B4c1b2c2
China	FJ026038	Irwin et al. (2009)	D5b
China	FJ026039	Irwin et al. (2009)	F1a1d
China	FJ026040	Irwin et al. (2009)	D4a7
China	FJ026041	Irwin et al. (2009)	F1a1c
China	FJ026042	Irwin et al. (2009)	R9b1a
China	FJ026043	Irwin et al. (2009)	B4c1b
China	FJ026044	Irwin et al. (2009)	M7c1c2
China	FJ026045	Irwin et al. (2009)	R9c1b1
China	FJ026046	Irwin et al. (2009)	B4d3
China	FJ026047	Irwin et al. (2009)	F2b1
China	FJ026048	Irwin et al. (2009)	B5a1d
China	FJ026049	Irwin et al. (2009)	D4a3
China	FJ026050	Irwin et al. (2009)	M9a1a
China	FJ026051	Irwin et al. (2009)	F1a1c
China	FJ026052	Irwin et al. (2009)	N9a1'3
China	FJ026053	Irwin et al. (2009)	R11
China	FJ026054	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026055	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026056	Irwin et al. (2009)	R9
China	FJ026057	Irwin et al. (2009)	Z+152
China	FJ026058	Irwin et al. (2009)	R9b2
China	FJ026059	Irwin et al. (2009)	D4a3
China	FJ026060	Irwin et al. (2009)	N9a4
China	FJ026061	Irwin et al. (2009)	A+152+16362+200
China	FJ026062	Irwin et al. (2009)	M8a2'3
China	FJ026063	Irwin et al. (2009)	B4b1a+207
China	FJ026064	Irwin et al. (2009)	D4e1a2
China	FJ026065	Irwin et al. (2009)	M10a1a1
China	FJ026066	Irwin et al. (2009)	Z4
China	FJ026067	Irwin et al. (2009)	F3a
China	FJ026068	Irwin et al. (2009)	D4a7
China	FJ026069	Irwin et al. (2009)	M7c1c2
China	FJ026070	Irwin et al. (2009)	F1e3

Population	GenBank	Reference	Haplogroup (HG)
China	FJ026071	Irwin et al. (2009)	F1a1a
China	FJ026072	Irwin et al. (2009)	M10a1a1b1
China	FJ026073	Irwin et al. (2009)	F1a1d
China	FJ026074	Irwin et al. (2009)	B4g
China	FJ026075	Irwin et al. (2009)	D5b
China	FJ026076	Irwin et al. (2009)	B6a
China	FJ026077	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026078	Irwin et al. (2009)	F1e3
China	FJ026079	Irwin et al. (2009)	B5a1d
China	FJ026080	Irwin et al. (2009)	M7c1c2
China	FJ026081	Irwin et al. (2009)	B4c1b+16335
China	FJ026082	Irwin et al. (2009)	Y1
China	FJ026083	Irwin et al. (2009)	F1a1a
China	FJ026084	Irwin et al. (2009)	D4e1
China	FJ026085	Irwin et al. (2009)	G1a
China	FJ026086	Irwin et al. (2009)	R9b1a
China	FJ026087	Irwin et al. (2009)	B5a
China	FJ026088	Irwin et al. (2009)	B4b1a+207
China	FJ026089	Irwin et al. (2009)	B5a
China	FJ026090	Irwin et al. (2009)	D5a2a1
China	FJ026091	Irwin et al. (2009)	F1a
China	FJ026092	Irwin et al. (2009)	B5a
China	FJ026093	Irwin et al. (2009)	F1a1a
China	FJ026094	Irwin et al. (2009)	J1d5
China	FJ026095	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026096	Irwin et al. (2009)	F2a
China	FJ026097	Irwin et al. (2009)	D5b
China	FJ026098	Irwin et al. (2009)	F2b1
China	FJ026099	Irwin et al. (2009)	D4e1
China	FJ026100	Irwin et al. (2009)	R11
China	FJ026101	Irwin et al. (2009)	N10a
China	FJ026102	Irwin et al. (2009)	B4h
China	FJ026103	Irwin et al. (2009)	M9a'b
China	FJ026104	Irwin et al. (2009)	R9b1
China	FJ026105	Irwin et al. (2009)	M7b1a1a
China	FJ026106	Irwin et al. (2009)	A11

Population	GenBank	Reference	Haplogroup (HG)
China	FJ026107	Irwin et al. (2009)	B4h1
China	FJ026108	Irwin et al. (2009)	B4g2
China	FJ026109	Irwin et al. (2009)	M7c2
China	FJ026110	Irwin et al. (2009)	F1a1d
China	FJ026111	Irwin et al. (2009)	B4c1b2c1
China	FJ026112	Irwin et al. (2009)	M7b1a1c
China	FJ026113	Irwin et al. (2009)	B5a
China	FJ026114	Irwin et al. (2009)	D1j1a2
China	FJ026115	Irwin et al. (2009)	F1a1a
China	FJ026116	Irwin et al. (2009)	D4a7
China	FJ026117	Irwin et al. (2009)	P4b
China	FJ026118	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026119	Irwin et al. (2009)	Z+152
China	FJ026120	Irwin et al. (2009)	D5a3
China	FJ026121	Irwin et al. (2009)	F1a1d
China	FJ026122	Irwin et al. (2009)	B5a
China	FJ026123	Irwin et al. (2009)	F1a1a
China	FJ026124	Irwin et al. (2009)	F1a1
China	FJ026125	Irwin et al. (2009)	D4e1
China	FJ026126	Irwin et al. (2009)	B4b1a+207
China	FJ026127	Irwin et al. (2009)	C4b1
China	FJ026128	Irwin et al. (2009)	B4h
China	FJ026129	Irwin et al. (2009)	M9a1a
China	FJ026130	Irwin et al. (2009)	F3a1
China	FJ026131	Irwin et al. (2009)	D4a7
China	FJ026132	Irwin et al. (2009)	F1c1a1
China	FJ026133	Irwin et al. (2009)	B4a1e
China	FJ026134	Irwin et al. (2009)	B4c1b
China	FJ026135	Irwin et al. (2009)	A5b1b
China	FJ026136	Irwin et al. (2009)	M7b1a1a
China	FJ026137	Irwin et al. (2009)	D4e1a
China	FJ026138	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026139	Irwin et al. (2009)	N10a
China	FJ026140	Irwin et al. (2009)	B5a
China	FJ026141	Irwin et al. (2009)	M7c1c2
China	FJ026142	Irwin et al. (2009)	B6a1

Population	GenBank	Reference	Haplogroup (HG)
China	FJ026143	Irwin et al. (2009)	B5a
China	FJ026144	Irwin et al. (2009)	D5b4
China	FJ026145	Irwin et al. (2009)	D4a3a2
China	FJ026146	Irwin et al. (2009)	D5b
China	FJ026147	Irwin et al. (2009)	B4a4
China	FJ026148	Irwin et al. (2009)	M7c1c2
China	FJ026149	Irwin et al. (2009)	M7b1a1e2
China	FJ026150	Irwin et al. (2009)	F1a
China	FJ026151	Irwin et al. (2009)	D5b
China	FJ026152	Irwin et al. (2009)	M33c
China	FJ026153	Irwin et al. (2009)	A+152+16362
China	FJ026154	Irwin et al. (2009)	D4g2a
China	FJ026155	Irwin et al. (2009)	G2a1d2
China	FJ026156	Irwin et al. (2009)	D4a
China	FJ026157	Irwin et al. (2009)	D5a2a1b1
China	FJ026158	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026159	Irwin et al. (2009)	B5a
China	FJ026160	Irwin et al. (2009)	B4b1a+207
China	FJ026161	Irwin et al. (2009)	F1a1
China	FJ026162	Irwin et al. (2009)	F4a1a
China	FJ026163	Irwin et al. (2009)	F3a1
China	FJ026164	Irwin et al. (2009)	F2i
China	FJ026165	Irwin et al. (2009)	R9c1b1
China	FJ026166	Irwin et al. (2009)	C4b8a
China	FJ026167	Irwin et al. (2009)	Z+152
China	FJ026168	Irwin et al. (2009)	B4a3
China	FJ026169	Irwin et al. (2009)	C4c1b
China	FJ026170	Irwin et al. (2009)	D5a2
China	FJ026171	Irwin et al. (2009)	F3a1
China	FJ026172	Irwin et al. (2009)	N10b
China	FJ026173	Irwin et al. (2009)	F1a1c
China	FJ026174	Irwin et al. (2009)	D4j1a
China	FJ026175	Irwin et al. (2009)	N10b
China	FJ026176	Irwin et al. (2009)	B4b1b'c
China	FJ026177	Irwin et al. (2009)	F1a4a1
China	FJ026178	Irwin et al. (2009)	D4b2b

Population	GenBank	Reference	Haplogroup (HG)
China	FJ026179	Irwin et al. (2009)	D4a7
China	FJ026180	Irwin et al. (2009)	M9
China	FJ026181	Irwin et al. (2009)	D5b1c1
China	FJ026182	Irwin et al. (2009)	F1a
China	FJ026183	Irwin et al. (2009)	F2a+@16291
China	FJ026184	Irwin et al. (2009)	M8a2'3
China	FJ026185	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026186	Irwin et al. (2009)	B5a
China	FJ026187	Irwin et al. (2009)	B4c1b2a
China	FJ026188	Irwin et al. (2009)	A5b1
China	FJ026189	Irwin et al. (2009)	F1a1
China	FJ026190	Irwin et al. (2009)	N10a
China	FJ026191	Irwin et al. (2009)	F2+16291
China	FJ026192	Irwin et al. (2009)	M9
China	FJ026193	Irwin et al. (2009)	M10a1a1b1
China	FJ026194	Irwin et al. (2009)	D4b1b
China	FJ026195	Irwin et al. (2009)	A11
China	FJ026196	Irwin et al. (2009)	F1a
China	FJ026197	Irwin et al. (2009)	F1a1
China	FJ026198	Irwin et al. (2009)	R9c1b1
China	FJ026199	Irwin et al. (2009)	F1a1d
China	FJ026200	Irwin et al. (2009)	M7c1c2
China	FJ026201	Irwin et al. (2009)	D4a3a2
China	FJ026202	Irwin et al. (2009)	M8
China	FJ026203	Irwin et al. (2009)	Y1
China	FJ026204	Irwin et al. (2009)	M7b1a1
China	FJ026205	Irwin et al. (2009)	M7b1a1b
China	FJ026206	Irwin et al. (2009)	B5a
China	FJ026207	Irwin et al. (2009)	F1a
China	FJ026208	Irwin et al. (2009)	F2b1
China	FJ026209	Irwin et al. (2009)	B5
China	FJ026210	Irwin et al. (2009)	B4c1b2a
China	FJ026211	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026212	Irwin et al. (2009)	H2a2a
China	FJ026213	Irwin et al. (2009)	R9c1b1
China	FJ026214	Irwin et al. (2009)	F1a1a

Population	GenBank	Reference	Haplogroup (HG)
China	FJ026215	Irwin et al. (2009)	M8a2a1
China	FJ026216	Irwin et al. (2009)	D4p
China	FJ026217	Irwin et al. (2009)	F1a2
China	FJ026218	Irwin et al. (2009)	B4b1b'c
China	FJ026219	Irwin et al. (2009)	M33c
China	FJ026220	Irwin et al. (2009)	F1a1a
China	FJ026221	Irwin et al. (2009)	D4a6
China	FJ026222	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026223	Irwin et al. (2009)	B4+16261
China	FJ026224	Irwin et al. (2009)	B5a
China	FJ026225	Irwin et al. (2009)	F1a1d
China	FJ026226	Irwin et al. (2009)	R9c1b1
China	FJ026227	Irwin et al. (2009)	F1a4a
China	FJ026228	Irwin et al. (2009)	D5b1b2
China	FJ026229	Irwin et al. (2009)	D6c
China	FJ026230	Irwin et al. (2009)	B5a
China	FJ026231	Irwin et al. (2009)	M7b1a1a3
China	FJ026232	Irwin et al. (2009)	D4a1e
China	FJ026233	Irwin et al. (2009)	M10a1+16129
China	FJ026234	Irwin et al. (2009)	B4b1b'c
China	FJ026235	Irwin et al. (2009)	M7b1a1b
China	FJ026236	Irwin et al. (2009)	D4a3a2
China	FJ026237	Irwin et al. (2009)	D4a3a2
China	FJ026238	Irwin et al. (2009)	M7c1
China	FJ026239	Irwin et al. (2009)	M7c1
China	FJ026240	Irwin et al. (2009)	D4a3
China	FJ026241	Irwin et al. (2009)	D4b1a1
China	FJ026242	Irwin et al. (2009)	M7b1a1
China	FJ026243	Irwin et al. (2009)	B4+16261
China	FJ026244	Irwin et al. (2009)	R9c1b1
China	FJ026245	Irwin et al. (2009)	C
China	FJ026246	Irwin et al. (2009)	R9b1a
China	FJ026247	Irwin et al. (2009)	B4h
China	FJ026248	Irwin et al. (2009)	F1a1c
China	FJ026249	Irwin et al. (2009)	M7b1a1
China	FJ026250	Irwin et al. (2009)	D4m2

Population	GenBank	Reference	Haplogroup (HG)
China	FJ026251	Irwin et al. (2009)	M74a
China	FJ026252	Irwin et al. (2009)	M
China	FJ026253	Irwin et al. (2009)	M7c1
China	FJ026254	Irwin et al. (2009)	D6c
China	FJ026255	Irwin et al. (2009)	B4a1c3
China	FJ026256	Irwin et al. (2009)	B4b1a+207
China	FJ026257	Irwin et al. (2009)	D4b2b
China	FJ026258	Irwin et al. (2009)	M7b1a1a1
China	FJ026259	Irwin et al. (2009)	A5b1b
China	FJ026260	Irwin et al. (2009)	F3a1
China	FJ026261	Irwin et al. (2009)	M7b1a1b
China	FJ026262	Irwin et al. (2009)	D4b2a2a
China	FJ026263	Irwin et al. (2009)	G2c
China	FJ026264	Irwin et al. (2009)	M7b1a1b
China	FJ026265	Irwin et al. (2009)	F4a1a
China	FJ026266	Irwin et al. (2009)	G2b2b
China	FJ026267	Irwin et al. (2009)	D4a3b2
China	FJ026268	Irwin et al. (2009)	F1a2
China	FJ026269	Irwin et al. (2009)	C4b8a
China	FJ026270	Irwin et al. (2009)	M7b1a1b
China	FJ026271	Irwin et al. (2009)	F1a1d
China	FJ026272	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026273	Irwin et al. (2009)	F1a
China	FJ026274	Irwin et al. (2009)	D4j1a
China	FJ026275	Irwin et al. (2009)	R9b1a1a
China	FJ026276	Irwin et al. (2009)	D5a3
China	FJ026277	Irwin et al. (2009)	R9b1
China	FJ026278	Irwin et al. (2009)	F1+16189
China	FJ026279	Irwin et al. (2009)	F3a1
China	FJ026280	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026281	Irwin et al. (2009)	M7b1a1b
China	FJ026282	Irwin et al. (2009)	R8a2
China	FJ026283	Irwin et al. (2009)	D4a3b2
China	FJ026284	Irwin et al. (2009)	A11
China	FJ026285	Irwin et al. (2009)	D4b2a2a
China	FJ026286	Irwin et al. (2009)	M7b1a1+(16192)

Population	GenBank	Reference	Haplogroup (HG)
China	FJ026287	Irwin et al. (2009)	F3a1
China	FJ026288	Irwin et al. (2009)	N9a
China	FJ026289	Irwin et al. (2009)	F2b1
China	FJ026290	Irwin et al. (2009)	B4
China	FJ026291	Irwin et al. (2009)	D5a2a1
China	FJ026292	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026293	Irwin et al. (2009)	R9b1
China	FJ026294	Irwin et al. (2009)	C4+152
China	FJ026295	Irwin et al. (2009)	D5a2a1
China	FJ026296	Irwin et al. (2009)	M7b1a1
China	FJ026297	Irwin et al. (2009)	M8a2a1
China	FJ026298	Irwin et al. (2009)	C4a1a+195
China	FJ026299	Irwin et al. (2009)	F1a1a
China	FJ026300	Irwin et al. (2009)	G1a
China	FJ026301	Irwin et al. (2009)	Y
China	FJ026302	Irwin et al. (2009)	D4j+(16286)
China	FJ026303	Irwin et al. (2009)	M71a1a
China	FJ026304	Irwin et al. (2009)	B4c1b2a
China	FJ026305	Irwin et al. (2009)	Z4a1
China	FJ026306	Irwin et al. (2009)	D5a2a1
China	FJ026307	Irwin et al. (2009)	D5a3
China	FJ026308	Irwin et al. (2009)	B5a
China	FJ026309	Irwin et al. (2009)	C4c1b
China	FJ026310	Irwin et al. (2009)	F1a1
China	FJ026311	Irwin et al. (2009)	M7b1a1b
China	FJ026312	Irwin et al. (2009)	F2a
China	FJ026313	Irwin et al. (2009)	M9a'b
China	FJ026314	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026315	Irwin et al. (2009)	F1a2
China	FJ026316	Irwin et al. (2009)	A+152+16362+200
China	FJ026317	Irwin et al. (2009)	D4a7
China	FJ026318	Irwin et al. (2009)	G2a1d
China	FJ026319	Irwin et al. (2009)	F1a1a
China	FJ026320	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026321	Irwin et al. (2009)	F1a3b
China	FJ026322	Irwin et al. (2009)	M9

Population	GenBank	Reference	Haplogroup (HG)
China	FJ026323	Irwin et al. (2009)	F3a1
China	FJ026324	Irwin et al. (2009)	M7c1
China	FJ026325	Irwin et al. (2009)	D6c
China	FJ026326	Irwin et al. (2009)	F1a
China	FJ026327	Irwin et al. (2009)	M74a
China	FJ026328	Irwin et al. (2009)	M10a1+16129
China	FJ026329	Irwin et al. (2009)	M71
China	FJ026330	Irwin et al. (2009)	A
China	FJ026331	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026332	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026333	Irwin et al. (2009)	D4g2a
China	FJ026334	Irwin et al. (2009)	M7c2
China	FJ026335	Irwin et al. (2009)	R9c1b1
China	FJ026336	Irwin et al. (2009)	A5b1b
China	FJ026337	Irwin et al. (2009)	B4c1c1
China	FJ026338	Irwin et al. (2009)	F1e3
China	FJ026339	Irwin et al. (2009)	M60a
China	FJ026340	Irwin et al. (2009)	M7b1a1a
China	FJ026341	Irwin et al. (2009)	N9a10+16311
China	FJ026342	Irwin et al. (2009)	F2b1
China	FJ026343	Irwin et al. (2009)	F1a1d
China	FJ026344	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026345	Irwin et al. (2009)	C1a
China	FJ026346	Irwin et al. (2009)	A5b1
China	FJ026347	Irwin et al. (2009)	M7b1a1a3
China	FJ026348	Irwin et al. (2009)	R11b1b
China	FJ026349	Irwin et al. (2009)	B5a
China	FJ026350	Irwin et al. (2009)	D4e1
China	FJ026351	Irwin et al. (2009)	M9
China	FJ026352	Irwin et al. (2009)	F2a+@16291
China	FJ026353	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026354	Irwin et al. (2009)	B4g2
China	FJ026355	Irwin et al. (2009)	D4j+146
China	FJ026356	Irwin et al. (2009)	M10a1+16129
China	FJ026357	Irwin et al. (2009)	B5a
China	FJ026358	Irwin et al. (2009)	B4h

Population	GenBank	Reference	Haplogroup (HG)
China	FJ026359	Irwin et al. (2009)	B5a
China	FJ026360	Irwin et al. (2009)	B4b1b'c
China	FJ026361	Irwin et al. (2009)	HV2
China	FJ026362	Irwin et al. (2009)	D4j3
China	FJ026363	Irwin et al. (2009)	A5b1b
China	FJ026364	Irwin et al. (2009)	M33c
China	FJ026365	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026366	Irwin et al. (2009)	M33c
China	FJ026367	Irwin et al. (2009)	F2a
China	FJ026368	Irwin et al. (2009)	B4c1b2a
China	FJ026369	Irwin et al. (2009)	F1c1a1
China	FJ026370	Irwin et al. (2009)	Z4
China	FJ026371	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026372	Irwin et al. (2009)	C
China	FJ026373	Irwin et al. (2009)	G2c
China	FJ026374	Irwin et al. (2009)	M7b1a1+(16192)
China	FJ026375	Irwin et al. (2009)	D4a7
China	FJ026376	Irwin et al. (2009)	C4b1
China	FJ026377	Irwin et al. (2009)	N9a10+16311
China	FJ026378	Irwin et al. (2009)	B5a
China	FJ026379	Irwin et al. (2009)	M33c
China	FJ026380	Irwin et al. (2009)	C4a1a+195
China	FJ026381	Irwin et al. (2009)	M9a'b
China	FJ026382	Irwin et al. (2009)	M7b1a1b
China	FJ026383	Irwin et al. (2009)	M7c1
China	FJ026384	Irwin et al. (2009)	D4j+(16286)
China	FJ026385	Irwin et al. (2009)	F1a1d
China	FJ026386	Irwin et al. (2009)	D4h4a
China	FJ026387	Irwin et al. (2009)	M9a5
China	FJ026388	Irwin et al. (2009)	M33a2'3
China	FJ026389	Irwin et al. (2009)	M7b1a1a1
China	FJ026390	Irwin et al. (2009)	M75
China	FJ026391	Irwin et al. (2009)	F2a+@16291
Chukchi	EF153803	Derenko et al. (2007)	A2a
Chukchi	EF153804	Derenko et al. (2007)	D2
Chukchi	EF153805	Derenko et al. (2007)	G1b

Population	GenBank	Reference	Haplogroup (HG)
Chukchi	EF153806	Derenko et al. (2007)	A2b
Chukchi	EF153807	Derenko et al. (2007)	A2b
Chukchi	EF153808	Derenko et al. (2007)	A2a
Chukchi	EF153809	Derenko et al. (2007)	A2b
Chukchi	EU007894	Ingman and Gyllensten (2007)	A2b1
Chukchi	EU007841	Ingman and Gyllensten (2007)	G1b2
Chukchi	EU007840	Ingman and Gyllensten (2007)	A2b1
Chukchi	EU007839	Ingman and Gyllensten (2007)	C4b2a
Chukchi	EU007838	Ingman and Gyllensten (2007)	A2a
Chukchi	EU007837	Ingman and Gyllensten (2007)	A2b1
Chukchi	EU007836	Ingman and Gyllensten (2007)	A2b1
Chukchi	EU007835	Ingman and Gyllensten (2007)	D2a2
Chukchi	AF346971	Ingman et al. (2000)	A2b1
Chukchi	GQ376202	Sukernik et al. (2012)	D3a2a1
Chukchi	EU482333	Volodko et al. (2008)	C2a
Chukchi	EU482338	Volodko et al. (2008)	A2a
Chukchi	EU482339	Volodko et al. (2008)	D2
Chuvash	JN857037	Derenko et al. (2012)	B4b1a3a1a
Chuvash	JN857036	Derenko et al. (2012)	B4b1a3a1a
Chuvash	JN857035	Derenko et al. (2012)	B4c1b2b
Chuvash	JQ245746	Fernandes et al. (2012)	I1a
Csango	EF185421	Brandstatter et al. (2007)	K1c
Csango	EF185422	Brandstatter et al. (2007)	H13a2c
Csango	EF185423	Brandstatter et al. (2007)	H1a1c
Csango	EF185424	Brandstatter et al. (2007)	U5a1+@16192
Csango	EF185425	Brandstatter et al. (2007)	A1a
Csango	EF185426	Brandstatter et al. (2007)	U8a1a
Csango	EF185427	Brandstatter et al. (2007)	K1a
Csango	EF185428	Brandstatter et al. (2007)	W3a1+199
Csango	EF185429	Brandstatter et al. (2007)	K1c
Csango	EF185430	Brandstatter et al. (2007)	J1c7
Csango	EF185431	Brandstatter et al. (2007)	J1c3+189
Csango	EF185432	Brandstatter et al. (2007)	K1c
Csango	EF185433	Brandstatter et al. (2007)	U4b3
Csango	EF185434	Brandstatter et al. (2007)	K1c
Csango	EF185435	Brandstatter et al. (2007)	J1c3+189

Population	GenBank	Reference	Haplogroup (HG)
Csango	EF185436	Brandstatter et al. (2007)	R0a2k1
Csango	EF185437	Brandstatter et al. (2007)	J1
Csango	EF185438	Brandstatter et al. (2007)	J1c3+189
Csango	EF185439	Brandstatter et al. (2007)	W3a1+199
Csango	EF185440	Brandstatter et al. (2007)	K1c
Csango	EF185441	Brandstatter et al. (2007)	W3a1+199
Csango	EF185442	Brandstatter et al. (2007)	K1c
Csango	EF185443	Brandstatter et al. (2007)	H11a2
Csango	EF185444	Brandstatter et al. (2007)	U5a1+@16192
Csango	EF185445	Brandstatter et al. (2007)	K1c
Csango	EF185446	Brandstatter et al. (2007)	I1a1
Csango	EF185447	Brandstatter et al. (2007)	J1c3+189
Csango	EF185448	Brandstatter et al. (2007)	J1c3+189
Csango	EF185449	Brandstatter et al. (2007)	W3a1+199
Csango	EF185450	Brandstatter et al. (2007)	U8b1a1
Csango	EF185451	Brandstatter et al. (2007)	H5b4
Csango	EF185452	Brandstatter et al. (2007)	K1c
Csango	EF185453	Brandstatter et al. (2007)	H1a1c
Csango	EF185454	Brandstatter et al. (2007)	U2d3
Csango	EF185455	Brandstatter et al. (2007)	H5b4
Csango	EF185456	Brandstatter et al. (2007)	U8a1a
Csango	EF185457	Brandstatter et al. (2007)	K1c
Csango	EF185458	Brandstatter et al. (2007)	K1c
Csango	EF185459	Brandstatter et al. (2007)	K1c
Csango	EF185460	Brandstatter et al. (2007)	K1c
Csango	EF185461	Brandstatter et al. (2007)	H14b1
Csango	EF185462	Brandstatter et al. (2007)	J1c3+189
Csango	EF185463	Brandstatter et al. (2007)	U5b1e
Csango	EF185464	Brandstatter et al. (2007)	W+194
Csango	EF185465	Brandstatter et al. (2007)	J1c3+189
Csango	EF185466	Brandstatter et al. (2007)	U8a1a
Csango	EF185467	Brandstatter et al. (2007)	W+194
Csango	EF185468	Brandstatter et al. (2007)	U5a1
Csango	EF185469	Brandstatter et al. (2007)	A1a
Csango	EF185470	Brandstatter et al. (2007)	T2b
Csango	EF185471	Brandstatter et al. (2007)	J1c3+189

Population	GenBank	Reference	Haplogroup (HG)
Csango	EF185472	Brandstatter et al. (2007)	K1c
Csango	EF185473	Brandstatter et al. (2007)	N1b1
Csango	EF185474	Brandstatter et al. (2007)	W+194
Csango	EF185475	Brandstatter et al. (2007)	X2e1b
Csango	EF185476	Brandstatter et al. (2007)	K1c
Csango	EF185477	Brandstatter et al. (2007)	HV0
Csango	EF185478	Brandstatter et al. (2007)	K1c
Csango	EF185479	Brandstatter et al. (2007)	J1c3+189
Csango	EF185480	Brandstatter et al. (2007)	H13a2c
Csango	EF185481	Brandstatter et al. (2007)	U5b1e
Csango	EF185482	Brandstatter et al. (2007)	J1c3+189
Csango	EF185483	Brandstatter et al. (2007)	H13a2c
Csango	EF185484	Brandstatter et al. (2007)	H6
Csango	EF185485	Brandstatter et al. (2007)	U4
Csango	EF185486	Brandstatter et al. (2007)	H1e+16129
Csango	EF185487	Brandstatter et al. (2007)	K1c
Csango	EF185488	Brandstatter et al. (2007)	K1c
Csango	EF185489	Brandstatter et al. (2007)	H11a1
Csango	EF185490	Brandstatter et al. (2007)	U5b
Csango	EF185491	Brandstatter et al. (2007)	H5
Csango	EF185492	Brandstatter et al. (2007)	N1b1
Csango	EF185493	Brandstatter et al. (2007)	HV0
Csango	EF185494	Brandstatter et al. (2007)	H1a1c
Csango	EF185495	Brandstatter et al. (2007)	W+194
Csango	EF185496	Brandstatter et al. (2007)	J1c3+189
Csango	EF185497	Brandstatter et al. (2007)	H5+16192
Csango	EF185498	Brandstatter et al. (2007)	N1b1
Csango	EF185499	Brandstatter et al. (2007)	H5
Csango	EF185500	Brandstatter et al. (2007)	J1c3j
Csango	EF185501	Brandstatter et al. (2007)	H1e+16129
Csango	EF185502	Brandstatter et al. (2007)	H1a1c
Csango	EF185503	Brandstatter et al. (2007)	U5a1
Csango	EF185504	Brandstatter et al. (2007)	U3a
Csango	EF185505	Brandstatter et al. (2007)	T2
Csango	EF185506	Brandstatter et al. (2007)	H66a
Csango	EF185507	Brandstatter et al. (2007)	K1a

Population	GenBank	Reference	Haplogroup (HG)
Csango	EF185508	Brandstatter et al. (2007)	W3a1+199
Csango	EF185509	Brandstatter et al. (2007)	T2+16189
Csango	EF185510	Brandstatter et al. (2007)	K1c
Csango	EF185511	Brandstatter et al. (2007)	I1a1
Csango	EF185512	Brandstatter et al. (2007)	N1b1
Csango	EF185513	Brandstatter et al. (2007)	K1c
Csango	EF185514	Brandstatter et al. (2007)	T1a+152
Csango	EF185515	Brandstatter et al. (2007)	K1c
Csango	EF185516	Brandstatter et al. (2007)	T2b
Csango	EF185517	Brandstatter et al. (2007)	K1c
Csango	EF185518	Brandstatter et al. (2007)	U5a2
Csango	EF185519	Brandstatter et al. (2007)	H1t1a1
Csango	EF185520	Brandstatter et al. (2007)	U2e2
Cyprus	DQ418040	Irwin et al. (2008)	U3
Cyprus	DQ418041	Irwin et al. (2008)	K1a8
Cyprus	DQ418042	Irwin et al. (2008)	W+194
Cyprus	DQ418043	Irwin et al. (2008)	X2e1
Cyprus	DQ418044	Irwin et al. (2008)	K1a8
Cyprus	DQ418045	Irwin et al. (2008)	L1c2
Cyprus	DQ418046	Irwin et al. (2008)	K1a4+146
Cyprus	DQ418047	Irwin et al. (2008)	U4c2a
Cyprus	DQ418048	Irwin et al. (2008)	J1c
Cyprus	DQ418049	Irwin et al. (2008)	U5a2
Cyprus	DQ418050	Irwin et al. (2008)	H1e5
Cyprus	DQ418051	Irwin et al. (2008)	U3a2a
Cyprus	DQ418052	Irwin et al. (2008)	H5n
Cyprus	DQ418053	Irwin et al. (2008)	H9a
Cyprus	DQ418054	Irwin et al. (2008)	T2i
Cyprus	DQ418055	Irwin et al. (2008)	U4c2a
Cyprus	DQ418056	Irwin et al. (2008)	J1b1a2
Cyprus	DQ418057	Irwin et al. (2008)	HV4a
Cyprus	DQ418058	Irwin et al. (2008)	U5a2
Cyprus	DQ418059	Irwin et al. (2008)	K1a
Cyprus	DQ418060	Irwin et al. (2008)	U1b3
Cyprus	DQ418061	Irwin et al. (2008)	K1a
Cyprus	DQ418062	Irwin et al. (2008)	H10+(16093)

Population	GenBank	Reference	Haplogroup (HG)
Cyprus	DQ418063	Irwin et al. (2008)	H15
Cyprus	DQ418064	Irwin et al. (2008)	K1a4a1a+195
Cyprus	DQ418065	Irwin et al. (2008)	H15
Cyprus	DQ418066	Irwin et al. (2008)	U7
Cyprus	DQ418067	Irwin et al. (2008)	H2a+152 16311
Cyprus	DQ418068	Irwin et al. (2008)	K1a
Cyprus	DQ418069	Irwin et al. (2008)	M1
Cyprus	DQ418070	Irwin et al. (2008)	K1a
Cyprus	DQ418071	Irwin et al. (2008)	L2a1c6
Cyprus	DQ418072	Irwin et al. (2008)	K1a1c
Cyprus	DQ418073	Irwin et al. (2008)	H2a2a
Cyprus	DQ418074	Irwin et al. (2008)	H2a2a
Cyprus	DQ418075	Irwin et al. (2008)	H2a2a
Cyprus	DQ418076	Irwin et al. (2008)	J2b
Cyprus	DQ418077	Irwin et al. (2008)	H9a
Cyprus	DQ418078	Irwin et al. (2008)	U3a2a
Cyprus	DQ418079	Irwin et al. (2008)	H1m1
Cyprus	DQ418080	Irwin et al. (2008)	T2c1+146
Cyprus	DQ418081	Irwin et al. (2008)	H5u
Cyprus	DQ418082	Irwin et al. (2008)	M1
Cyprus	DQ418083	Irwin et al. (2008)	K1a4c
Cyprus	DQ418084	Irwin et al. (2008)	T2f7a
Cyprus	DQ418085	Irwin et al. (2008)	H7c1
Cyprus	DQ418086	Irwin et al. (2008)	I1
Cyprus	DQ418087	Irwin et al. (2008)	H1+152
Cyprus	DQ418088	Irwin et al. (2008)	K1a4+146
Cyprus	DQ418089	Irwin et al. (2008)	R8a1a2
Cyprus	DQ418090	Irwin et al. (2008)	H2a2a
Cyprus	DQ418091	Irwin et al. (2008)	K1a
Cyprus	DQ418092	Irwin et al. (2008)	H14a
Cyprus	DQ418093	Irwin et al. (2008)	T2c1f
Cyprus	DQ418094	Irwin et al. (2008)	T2c1f
Cyprus	DQ418095	Irwin et al. (2008)	K2a1a
Cyprus	DQ418096	Irwin et al. (2008)	K1b1c
Cyprus	DQ418097	Irwin et al. (2008)	J1c2h
Cyprus	DQ418098	Irwin et al. (2008)	K1a4+146

Population	GenBank	Reference	Haplogroup (HG)
Cyprus	DQ418099	Irwin et al. (2008)	H33b
Cyprus	DQ418100	Irwin et al. (2008)	I5c
Cyprus	DQ418101	Irwin et al. (2008)	H13a2b3
Cyprus	DQ418102	Irwin et al. (2008)	H7c1
Cyprus	DQ418103	Irwin et al. (2008)	U3
Cyprus	DQ418104	Irwin et al. (2008)	H2a2a
Cyprus	DQ418105	Irwin et al. (2008)	H1e2c
Cyprus	DQ418106	Irwin et al. (2008)	H42a
Cyprus	DQ418107	Irwin et al. (2008)	H2a1
Cyprus	DQ418108	Irwin et al. (2008)	L1b
Cyprus	DQ418109	Irwin et al. (2008)	K1a
Cyprus	DQ418110	Irwin et al. (2008)	X2e1
Cyprus	DQ418111	Irwin et al. (2008)	K1a1
Cyprus	DQ418112	Irwin et al. (2008)	W
Cyprus	DQ418113	Irwin et al. (2008)	N1b1
Cyprus	DQ418114	Irwin et al. (2008)	J2a1a2
Cyprus	DQ418115	Irwin et al. (2008)	R2b1
Cyprus	DQ418116	Irwin et al. (2008)	U3b2a1a
Cyprus	DQ418117	Irwin et al. (2008)	X2e1b
Cyprus	DQ418118	Irwin et al. (2008)	H3am
Cyprus	DQ418119	Irwin et al. (2008)	T2g1a1
Cyprus	DQ418120	Irwin et al. (2008)	H2a1
Cyprus	DQ418121	Irwin et al. (2008)	I5c1
Cyprus	DQ418122	Irwin et al. (2008)	H42a
Cyprus	DQ418123	Irwin et al. (2008)	H33b
Cyprus	DQ418124	Irwin et al. (2008)	K1a29a
Cyprus	DQ418125	Irwin et al. (2008)	R2b1
Cyprus	DQ418126	Irwin et al. (2008)	U1b3
Cyprus	DQ418127	Irwin et al. (2008)	K1a2a1
Cyprus	DQ418128	Irwin et al. (2008)	H14a
Cyprus	DQ418129	Irwin et al. (2008)	T2c1f
Cyprus	DQ418130	Irwin et al. (2008)	W+194
Czech Republic	JQ798097	Pala et al. (2012)	T2c1b2
Czech Republic	JX307105	Mielnik-Sikorska et al. (2013)	H6a1a
Czech	JX307106	Mielnik-Sikorska et al. (2013)	H6c

Population	GenBank	Reference	Haplogroup (HG)
Republic			
Czech Republic	JX307108	Mielnik-Sikorska et al. (2013)	H6a1b3
Czech Republic	JX128046	Mielnik-Sikorska et al. (2013)	H5b5
Czech Republic	JX128047	Mielnik-Sikorska et al. (2013)	H5a9
Czech Republic	JX128048	Mielnik-Sikorska et al. (2013)	H5
Czech Republic	JX128049	Mielnik-Sikorska et al. (2013)	H5b5
Czech Republic	JX128050	Mielnik-Sikorska et al. (2013)	H5b
Czech Republic	EU200760	Malyarchuk et al. (2008)	L2a1a
Czech Republic	JN857038	Derenko et al. (2012)	N9a3a
Czech Republic	FJ951557	Derenko et al. (2010)	D4e1b
Czech Republic	EU545427.2	Malyarchuk et al. (2008a)	U4a1
Czech Republic	EU545426.2	Malyarchuk et al. (2008a)	U4d
Czech Republic	EU545425.2	Malyarchuk et al. (2008a)	U4a2
Czech Republic	EU545423.2	Malyarchuk et al. (2008a)	U4a3
Czech Republic	EU545421.2	Malyarchuk et al. (2008a)	U4a2
Czech Republic	EU545424	Malyarchuk et al. (2008a)	HV3
Czech Republic	EU545422	Malyarchuk et al. (2008a)	HV3a
Czech Republic	EU545420	Malyarchuk et al. (2008a)	HV3a
Dargin	AM263179	Roostalu et al. (2007)	H2a4
Dargin	AM263180	Roostalu et al. (2007)	H2a3
Dargin	AM263181	Roostalu et al. (2007)	H2a4
Dubai	JQ797786	Pala et al. (2012)	J1b
Dubai	JQ798088	Pala et al. (2012)	T2b
Dubai	JQ798103	Pala et al. (2012)	T2c1c
Dubai	JQ245725	Fernandes et al. (2012)	N1b1b
Dubai	JQ245728	Fernandes et al. (2012)	W6

Population	GenBank	Reference	Haplogroup (HG)
Dubai	JQ245729	Fernandes et al. (2012)	N1c
Dubai	JQ245731	Fernandes et al. (2012)	X2
Dubai	JQ245732	Fernandes et al. (2012)	X2
Dubai	JQ245733	Fernandes et al. (2012)	I5a
Dubai	JQ245734	Fernandes et al. (2012)	N1e'I
Dubai	JQ245735	Fernandes et al. (2012)	N1e'I
Dubai	KP407056	Gandini et al. (unpub)	R0a2f
Estonia	JQ797978	Pala et al. (2012)	T1a1a1
Estonia	JQ797986	Pala et al. (2012)	T1a1a1
Estonia	JQ798077	Pala et al. (2012)	T2b16
Estonia	KF142470	direct submission	W3a1-T199C
Estonia	GQ129164	Pala et al. (2009)	U5b3a2
Estonia	JQ797819	Pala et al. (2012)	J1c2a
Estonia	JQ797828	Pala et al. (2012)	J1c3f
Even	FJ951558	Derenko et al. (2010)	D3
Even	FJ951559	Derenko et al. (2010)	C4b1
Even	FJ951560	Derenko et al. (2010)	C5a1
Even	FJ951561	Derenko et al. (2010)	C4b*
Even	FJ951562	Derenko et al. (2010)	C5a1
Even	EF153802	Derenko et al. (2007)	G1a1b
Even	HM776715	Sukernik et al. (2012)	Y1a
Even	FJ858889	Sukernik et al. (2012)	D4c2b
Even	FJ858888	Sukernik et al. (2012)	D6
Even	FJ858887	Sukernik et al. (2012)	D6
Even	FJ858883	Sukernik et al. (2012)	D3a1
Even	FJ858882	Sukernik et al. (2012)	D2c
Even	FJ858879	Sukernik et al. (2012)	D2b
Evenki	FJ951563	Derenko et al. (2010)	C6a
Evenki	FJ951564	Derenko et al. (2010)	D4e3a
Evenki	FJ951565	Derenko et al. (2010)	D4m1
Evenki	FJ951566	Derenko et al. (2010)	C5b1a
Evenki	FJ951567	Derenko et al. (2010)	D5a2b
Evenki	FJ951568	Derenko et al. (2010)	C4b1
Evenki	FJ951569	Derenko et al. (2010)	D4e3a
Evenki	FJ951570	Derenko et al. (2010)	D4l
Evenki	FJ951571	Derenko et al. (2010)	D4e3a

Population	GenBank	Reference	Haplogroup (HG)
Evenki	FJ951572	Derenko et al. (2010)	C4a2a1
Evenki	EF397560	Derenko et al. (2007)	A4b
Evenki	AF346979	Ingman et al. (2000)	C4a2a1b
Evenki	AY519485.2	Starikovskaya et al. (2005)	C4a2a1b
Evenki	AY195753.2	Mishmar et al. (2003)	C4a1a+195
Evenki	FJ493515	Sukernik et al. (2012)	Z1a
Evenki	EU482359	Volodko et al. (2008)	C4
Evenki	EU482360	Volodko et al. (2008)	D6
Evenki	EU482361	Volodko et al. (2008)	C2b
Evenki	EU482373	Volodko et al. (2008)	D5a1
Georgia	JQ797896	Pala et al. (2012)	J1d2c
Georgia	JQ798037	Pala et al. (2012)	T1b1
Georgia	HM852875	Schoenberg et al. (2011)	U4
Georgia	HM852876	Schoenberg et al. (2011)	R0
Georgia	HM852877	Schoenberg et al. (2011)	H+73
Georgia	HM852878	Schoenberg et al. (2011)	H2+152
Georgia	HM852879	Schoenberg et al. (2011)	T2b
Georgia	HM852880	Schoenberg et al. (2011)	H7
Georgia	HM852881	Schoenberg et al. (2011)	T2i
Georgia	HM852882	Schoenberg et al. (2011)	U1a1a1
Georgia	HM852883	Schoenberg et al. (2011)	K1b1c
Georgia	HM852884	Schoenberg et al. (2011)	U4b1b1
Georgia	HM852885	Schoenberg et al. (2011)	U4a2
Georgia	HM852886	Schoenberg et al. (2011)	K3
Georgia	HM852887	Schoenberg et al. (2011)	R1a
Georgia	HM852888	Schoenberg et al. (2011)	H10a1
Georgia	HM852889	Schoenberg et al. (2011)	H13a1a1
Georgia	HM852890	Schoenberg et al. (2011)	K1a4i
Georgia	HM852891	Schoenberg et al. (2011)	U3a
Georgia	HM852892	Schoenberg et al. (2011)	R1a1b
Han	AY963573.2	Macaulay et al. (2005)	D4b2b
Han	FJ748704	Ji et al. (2012)	M13a1b
Han	FJ748705	Ji et al. (2012)	A6b
Han	FJ748706	Ji et al. (2012)	M7b1a1+(16192)
Han	FJ748707	Ji et al. (2012)	G1c1
Han	FJ748708	Ji et al. (2012)	N9a1a

Population	GenBank	Reference	Haplogroup (HG)
Han	FJ748709	Ji et al. (2012)	M45
Han	FJ748710	Ji et al. (2012)	Z4a1a
Han	FJ748711	Ji et al. (2012)	C7a
Han	FJ748712	Ji et al. (2012)	F3a1
Han	FJ748713	Ji et al. (2012)	F1g1
Han	FJ748714	Ji et al. (2012)	A11b
Han	FJ748715	Ji et al. (2012)	M7c1c
Han	FJ748719	Ji et al. (2012)	N9a10+16311
Han	FJ748720	Ji et al. (2012)	F1c1a2
Han	FJ748721	Ji et al. (2012)	R11b
Hungary	DQ359555	Irwin et al. (2007)	J1c
Hungary	DQ359478	Irwin et al. (2007)	U5a1+@16192
Hungary	DQ359479	Irwin et al. (2007)	U4a1
Hungary	DQ359480	Irwin et al. (2007)	H4a1a+195
Hungary	DQ359481	Irwin et al. (2007)	T2+16189
Hungary	DQ359482	Irwin et al. (2007)	W3a1+199
Hungary	DQ359483	Irwin et al. (2007)	U4c1
Hungary	DQ359484	Irwin et al. (2007)	J1
Hungary	DQ359485	Irwin et al. (2007)	J1c2
Hungary	DQ359486	Irwin et al. (2007)	H1e1a4
Hungary	DQ359487	Irwin et al. (2007)	U1a1a2
Hungary	DQ359488	Irwin et al. (2007)	H1b
Hungary	DQ359489	Irwin et al. (2007)	H5
Hungary	DQ359490	Irwin et al. (2007)	H1a
Hungary	DQ359491	Irwin et al. (2007)	J1c2
Hungary	DQ359492	Irwin et al. (2007)	X2b10a
Hungary	DQ359493	Irwin et al. (2007)	H2a2a
Hungary	DQ359494	Irwin et al. (2007)	J1b1a1
Hungary	DQ359495	Irwin et al. (2007)	W+194
Hungary	DQ359496	Irwin et al. (2007)	H66a
Hungary	DQ359497	Irwin et al. (2007)	J2b1a6
Hungary	DQ359498	Irwin et al. (2007)	H1b2
Hungary	DQ359499	Irwin et al. (2007)	T1a2a
Hungary	DQ359500	Irwin et al. (2007)	U5b2a1a2
Hungary	DQ359501	Irwin et al. (2007)	T2b7a3
Hungary	DQ359502	Irwin et al. (2007)	H2a+152 16311

Population	GenBank	Reference	Haplogroup (HG)
Hungary	DQ359503	Irwin et al. (2007)	T2b
Hungary	DQ359504	Irwin et al. (2007)	H1b1+16362
Hungary	DQ359505	Irwin et al. (2007)	H3v+16093
Hungary	DQ359506	Irwin et al. (2007)	H2a1
Hungary	DQ359507	Irwin et al. (2007)	HV0+195
Hungary	DQ359508	Irwin et al. (2007)	I1a1
Hungary	DQ359509	Irwin et al. (2007)	H2a2a
Hungary	DQ359510	Irwin et al. (2007)	H2a2a
Hungary	DQ359511	Irwin et al. (2007)	J2b1a6
Hungary	DQ359512	Irwin et al. (2007)	H2a2a+(16235)
Hungary	DQ359513	Irwin et al. (2007)	J2b1a6
Hungary	DQ359514	Irwin et al. (2007)	U6a7a
Hungary	DQ359515	Irwin et al. (2007)	H24
Hungary	DQ359516	Irwin et al. (2007)	U2e1'2'3
Hungary	DQ359517	Irwin et al. (2007)	H5a5
Hungary	DQ359518	Irwin et al. (2007)	M5a1
Hungary	DQ359519	Irwin et al. (2007)	M5a1
Hungary	DQ359520	Irwin et al. (2007)	T
Hungary	DQ359521	Irwin et al. (2007)	U2e1
Hungary	DQ359522	Irwin et al. (2007)	M9
Hungary	DQ359523	Irwin et al. (2007)	H2a2a
Hungary	DQ359524	Irwin et al. (2007)	L2a1+143
Hungary	DQ359525	Irwin et al. (2007)	X4
Hungary	DQ359526	Irwin et al. (2007)	H1c3a
Hungary	DQ359527	Irwin et al. (2007)	T2b
Hungary	DQ359528	Irwin et al. (2007)	HV0+195
Hungary	DQ359529	Irwin et al. (2007)	T1a+152
Hungary	DQ359530	Irwin et al. (2007)	H12a
Hungary	DQ359531	Irwin et al. (2007)	T2f3
Hungary	DQ359532	Irwin et al. (2007)	H1e1a4
Hungary	DQ359533	Irwin et al. (2007)	T
Hungary	DQ359534	Irwin et al. (2007)	K1a4c1
Hungary	DQ359535	Irwin et al. (2007)	HV0
Hungary	DQ359536	Irwin et al. (2007)	H2a2a
Hungary	DQ359537	Irwin et al. (2007)	H1e+16129
Hungary	DQ359538	Irwin et al. (2007)	U5b1d1b

Population	GenBank	Reference	Haplogroup (HG)
Hungary	DQ359539	Irwin et al. (2007)	T2b3+151
Hungary	DQ359540	Irwin et al. (2007)	H3h4
Hungary	DQ359541	Irwin et al. (2007)	H5a3
Hungary	DQ359542	Irwin et al. (2007)	HV4a
Hungary	DQ359543	Irwin et al. (2007)	H2a2a
Hungary	DQ359544	Irwin et al. (2007)	H2a2a
Hungary	DQ359545	Irwin et al. (2007)	H1e1a1
Hungary	DQ359546	Irwin et al. (2007)	U2e2
Hungary	DQ359547	Irwin et al. (2007)	T1a4
Hungary	DQ359548	Irwin et al. (2007)	H1bv1
Hungary	DQ359549	Irwin et al. (2007)	T
Hungary	DQ359550	Irwin et al. (2007)	J1
Hungary	DQ359551	Irwin et al. (2007)	I3a
Hungary	DQ359552	Irwin et al. (2007)	T2e1
Hungary	DQ359553	Irwin et al. (2007)	U4b1+146 152
Hungary	DQ359554	Irwin et al. (2007)	H2a2a2
Hungary	DQ359556	Irwin et al. (2007)	U5b3
Hungary	DQ359557	Irwin et al. (2007)	K1b2
Hungary	DQ359558	Irwin et al. (2007)	T2
Hungary	DQ359559	Irwin et al. (2007)	H13a1d
Hungary	DQ359560	Irwin et al. (2007)	U5b1e
Hungary	DQ359561	Irwin et al. (2007)	H1e1a8
Hungary	DQ359562	Irwin et al. (2007)	U3
Hungary	DQ359563	Irwin et al. (2007)	H1af
Hungary	DQ359564	Irwin et al. (2007)	H2a1
Hungary	DQ359565	Irwin et al. (2007)	HV0
Hungary	DQ359566	Irwin et al. (2007)	HV4a
Hungary	DQ359567	Irwin et al. (2007)	W1+119
Hungary	DQ359568	Irwin et al. (2007)	H10+(16093)
Hungary	DQ359569	Irwin et al. (2007)	HV0
Hungary	DQ359570	Irwin et al. (2007)	K1a
Hungary	DQ359571	Irwin et al. (2007)	U4a1
Hungary	DQ359572	Irwin et al. (2007)	U4a1
Hungary	DQ359573	Irwin et al. (2007)	H2a5a1
Hungary	DQ359574	Irwin et al. (2007)	H3z
Hungary	DQ359575	Irwin et al. (2007)	H33c

Population	GenBank	Reference	Haplogroup (HG)
Hungary	DQ359576	Irwin et al. (2007)	H2a2a
Hungary	DQ359577	Irwin et al. (2007)	H10+(16093)
Hungary	DQ359578	Irwin et al. (2007)	H1m1
Hungary	DQ359579	Irwin et al. (2007)	H2a2a
Hungary	DQ359580	Irwin et al. (2007)	U5a1f2
Hungary	DQ359581	Irwin et al. (2007)	T2b
Hungary	DQ359582	Irwin et al. (2007)	H2a2a
Hungary	DQ359583	Irwin et al. (2007)	H2a2a
Hungary	DQ359584	Irwin et al. (2007)	U4b1a1a1
Hungary	DQ359585	Irwin et al. (2007)	H1e1a6
Hungary	DQ359586	Irwin et al. (2007)	H13a1a2a
Hungary	DQ359587	Irwin et al. (2007)	T2c1f
Hungary	DQ359588	Irwin et al. (2007)	H2a2a
Hungary	DQ359589	Irwin et al. (2007)	I3a
Hungary	DQ359590	Irwin et al. (2007)	X2d1
Hungary	DQ359591	Irwin et al. (2007)	H1a3
Hungary	DQ359592	Irwin et al. (2007)	H1+152
Hungary	DQ359593	Irwin et al. (2007)	T2a1b
Hungary	DQ359594	Irwin et al. (2007)	T2b4a
Hungary	DQ359595	Irwin et al. (2007)	H1+16239
Hungary	DQ359596	Irwin et al. (2007)	R0a2i
Hungary	DQ359597	Irwin et al. (2007)	HV0
Hungary	DQ359598	Irwin et al. (2007)	T2c1a
Hungary	DQ359599	Irwin et al. (2007)	K1c2
Hungary	DQ359600	Irwin et al. (2007)	J1
Hungary	DQ359601	Irwin et al. (2007)	HV0
Hungary	DQ359602	Irwin et al. (2007)	U5b1b1a
Hungary	DQ359603	Irwin et al. (2007)	T
Hungary	DQ359604	Irwin et al. (2007)	K1a4a1a+195
Hungary	DQ359605	Irwin et al. (2007)	R0a1a
Hungary	DQ359606	Irwin et al. (2007)	H14b1
Hungary	DQ359607	Irwin et al. (2007)	H1+152
Hungary	DQ359608	Irwin et al. (2007)	K2b1b
Hungary	DQ359609	Irwin et al. (2007)	H1m1
Hungary	DQ359610	Irwin et al. (2007)	N1b1
Hungary	DQ359611	Irwin et al. (2007)	T1a

Population	GenBank	Reference	Haplogroup (HG)
Hungary	DQ359612	Irwin et al. (2007)	U4
Hungary	DQ359613	Irwin et al. (2007)	I1
Hungary	DQ359614	Irwin et al. (2007)	H5
Hungary	DQ359615	Irwin et al. (2007)	T2b3d
Hungary	DQ359616	Irwin et al. (2007)	H2a2a1
Hungary	DQ359617	Irwin et al. (2007)	H2a2a
Hungary	DQ359618	Irwin et al. (2007)	J1
Hungary	DQ359619	Irwin et al. (2007)	U8a1a
Hungary	DQ359620	Irwin et al. (2007)	T2a1b
Hungary	DQ359621	Irwin et al. (2007)	T2e1
Hungary	DQ359622	Irwin et al. (2007)	U4'9
Hungary	DQ359623	Irwin et al. (2007)	H6
Hungary	DQ359624	Irwin et al. (2007)	U5b1b1+@16192
Hungary	DQ359625	Irwin et al. (2007)	H2a2a
Hungary	DQ359626	Irwin et al. (2007)	N1b1
Hungary	DQ359627	Irwin et al. (2007)	U5b1e
Hungary	DQ359628	Irwin et al. (2007)	H1e+16129
Hungary	DQ359629	Irwin et al. (2007)	J2b1a6
Hungary	DQ359630	Irwin et al. (2007)	T2b24
Hungary	DQ359631	Irwin et al. (2007)	H5a1j
Hungary	DQ359632	Irwin et al. (2007)	H2a2a
Hungary	DQ359633	Irwin et al. (2007)	H7a1
Hungary	DQ359634	Irwin et al. (2007)	H1e5
Hungary	DQ359635	Irwin et al. (2007)	I4a1
Hungary	DQ359636	Irwin et al. (2007)	H2a2a
Hungary	DQ359637	Irwin et al. (2007)	H85
Hungary	DQ359638	Irwin et al. (2007)	W+194
Hungary	DQ359639	Irwin et al. (2007)	T2
Hungary	DQ359640	Irwin et al. (2007)	U5b2a1b
Hungary	DQ359641	Irwin et al. (2007)	H5
Hungary	DQ359642	Irwin et al. (2007)	K1a9
Hungary	DQ359643	Irwin et al. (2007)	M9
Hungary	DQ359644	Irwin et al. (2007)	U5a1b+16362
Hungary	DQ359645	Irwin et al. (2007)	J1b1b2
Hungary	DQ359646	Irwin et al. (2007)	J1b1a1
Hungary	DQ359647	Irwin et al. (2007)	T2b

Population	GenBank	Reference	Haplogroup (HG)
Hungary	DQ359648	Irwin et al. (2007)	K1a1b2a
Hungary	DQ359649	Irwin et al. (2007)	J2a1a
Hungary	DQ359650	Irwin et al. (2007)	J1c2
Hungary	DQ359651	Irwin et al. (2007)	H11a
Hungary	DQ359652	Irwin et al. (2007)	HV1b2
Hungary	DQ359653	Irwin et al. (2007)	J1
Hungary	DQ359654	Irwin et al. (2007)	U5a1+@16192
Hungary	DQ359655	Irwin et al. (2007)	T2g1
Hungary	DQ359656	Irwin et al. (2007)	H1+16189
Hungary	DQ359657	Irwin et al. (2007)	J2b1a6
Hungary	DQ359658	Irwin et al. (2007)	U5a1b1
Hungary	DQ359659	Irwin et al. (2007)	H11
Hungary	DQ359660	Irwin et al. (2007)	H2a2a
Hungary	DQ359661	Irwin et al. (2007)	U5a1a1d
Hungary	DQ359662	Irwin et al. (2007)	H7c1
Hungary	DQ359663	Irwin et al. (2007)	H1a1
Hungary	DQ359664	Irwin et al. (2007)	H5a4
Hungary	DQ359665	Irwin et al. (2007)	U5a2
Hungary	DQ359666	Irwin et al. (2007)	T1b
Hungary	DQ359667	Irwin et al. (2007)	U3
Hungary	DQ359668	Irwin et al. (2007)	HV0+195
Hungary	DQ359669	Irwin et al. (2007)	K1a4c
Hungary	DQ359670	Irwin et al. (2007)	H1c1b
Hungary	DQ359671	Irwin et al. (2007)	X2b11
Hungary	DQ359672	Irwin et al. (2007)	H5a5
Hungary	DQ359673	Irwin et al. (2007)	H6a1a2a
Hungary	DQ359674	Irwin et al. (2007)	T2
Hungary	DQ359675	Irwin et al. (2007)	J1b1b
Hungary	DQ359676	Irwin et al. (2007)	W6
Hungary	DQ359677	Irwin et al. (2007)	H2a+152 16311
Hungary	DQ359678	Irwin et al. (2007)	H1c
Hungary	DQ359679	Irwin et al. (2007)	W+194
Hungary	DQ359680	Irwin et al. (2007)	U5a1+@16192
Hungary	DQ359681	Irwin et al. (2007)	I1a1
Hungary	DQ359682	Irwin et al. (2007)	H2a2a
Hungary	DQ359683	Irwin et al. (2007)	J1b1a1

Population	GenBank	Reference	Haplogroup (HG)
Hungary	DQ359684	Irwin et al. (2007)	H7f
Hungary	DQ359685	Irwin et al. (2007)	U5b1d1b
Hungary	DQ359686	Irwin et al. (2007)	J2b1a
Hungary	DQ359687	Irwin et al. (2007)	U7
Hungary	DQ359688	Irwin et al. (2007)	H5
India	FJ383177	Kumar et al. (2009)	D4j1b
India	FJ383178	Kumar et al. (2009)	D4j1b
India	FJ383179	Kumar et al. (2009)	D4g2a1c
India	FJ383180	Kumar et al. (2009)	D5a2a1+@16172
India	FJ383181	Kumar et al. (2009)	D4j6
India	FJ383182	Kumar et al. (2009)	D4a1e
India	FJ383183	Kumar et al. (2009)	D4j1a1
India	FJ383184	Kumar et al. (2009)	D4j1a1
India	FJ383185	Kumar et al. (2009)	D4j1a1
India	FJ383186	Kumar et al. (2009)	D4j1a1
India	FJ383187	Kumar et al. (2009)	D4b2b5
India	FJ383188	Kumar et al. (2009)	D4j1a1a
India	FJ383189	Kumar et al. (2009)	D4j1a1a
India	FJ383190	Kumar et al. (2009)	D5a2a1+@16172
India	FJ383191	Kumar et al. (2009)	D4b2b5
India	FJ383192	Kumar et al. (2009)	D4b2b5
India	FJ383193	Kumar et al. (2009)	D4j1a1a
India	FJ383194	Kumar et al. (2009)	D4j1a1a
India	FJ383195	Kumar et al. (2009)	D5a2a1b
India	FJ383196	Kumar et al. (2009)	D4j1a1a
Iran	JQ797766	Pala et al. (2012)	J1b1b1a
Iran	JQ797768	Pala et al. (2012)	J1b1b1
Iran	JQ797770	Pala et al. (2012)	J1b1b
Iran	JQ797893	Pala et al. (2012)	J1d2a1
Iran	JQ797901	Pala et al. (2012)	J1d2e
Iran	JQ797973	Pala et al. (2012)	J2b2
Iran	JQ797993	Pala et al. (2012)	T1a1a1b1
Iran	JQ797995	Pala et al. (2012)	T1a1a1b1
Iran	JQ797998	Pala et al. (2012)	T1a1a1
Iran	JQ797999	Pala et al. (2012)	T1a1a1
Iran	JQ798000	Pala et al. (2012)	T1a1a1

Population	GenBank	Reference	Haplogroup (HG)
Iran	JQ798034	Pala et al. (2012)	T1a4a
Iran	JQ798042	Pala et al. (2012)	T1b3
Iran	JQ798072	Pala et al. (2012)	T2b5
Iran	JQ798076	Pala et al. (2012)	T2b23
Iran	JQ798098	Pala et al. (2012)	T2c1b2
Iran	JQ798108	Pala et al. (2012)	T2d2
Iran	JQ798131	Pala et al. (2012)	T2i
Iran	HM852816	Schoenberg et al. (2011)	HV18
Iran	HM852817	Schoenberg et al. (2011)	I5b1
Iraq	JQ995803	Al-Zahery et al. (2013)	K1a2a1
Iraq	JQ995804	Al-Zahery et al. (2013)	U1a1a
Iraq	JQ995805	Al-Zahery et al. (2013)	J1d
Iraq	JQ995806	Al-Zahery et al. (2013)	T2c1c
Iraq	JQ995807	Al-Zahery et al. (2013)	HV12a
Iraq	JQ995808	Al-Zahery et al. (2013)	X2d
Iraq	JQ995809	Al-Zahery et al. (2013)	HV12a
Iraq	JQ995810	Al-Zahery et al. (2013)	T1a1'3
Iraq	JQ995811	Al-Zahery et al. (2013)	HV12a
Iraq	JQ995812	Al-Zahery et al. (2013)	HV12a
Iraq	JQ995813	Al-Zahery et al. (2013)	HV12a
Iraq	JQ995814	Al-Zahery et al. (2013)	T1a1'3
Iraq	JQ995815	Al-Zahery et al. (2013)	T1a1'3
Iraq	JQ995816	Al-Zahery et al. (2013)	T2c1
Iraq	JQ995817	Al-Zahery et al. (2013)	T2c1
Iraq	JQ995818	Al-Zahery et al. (2013)	HV12a
Iraq	JQ995819	Al-Zahery et al. (2013)	T1a1'3
Iraq	JQ995820	Al-Zahery et al. (2013)	U5b2a1a2
Iraq	JQ995821	Al-Zahery et al. (2013)	U4
Iraq	JQ995822	Al-Zahery et al. (2013)	R0a1a
Iraq	JQ995823	Al-Zahery et al. (2013)	L1c2b2
Iraq	JQ995824	Al-Zahery et al. (2013)	J1d1a
Iraq	JQ995825	Al-Zahery et al. (2013)	H2a2a
Iraq	JQ995826	Al-Zahery et al. (2013)	H14a+146
Iraq	JQ995827	Al-Zahery et al. (2013)	H4a1a+195
Iraq	JQ995828	Al-Zahery et al. (2013)	T1
Iraq	JQ995829	Al-Zahery et al. (2013)	J1d

Population	GenBank	Reference	Haplogroup (HG)
Iraq	JQ995830	Al-Zahery et al. (2013)	T2
Iraq	JQ995831	Al-Zahery et al. (2013)	J1b
Iraq	JQ995832	Al-Zahery et al. (2013)	T2b3a1
Iraq	JQ995833	Al-Zahery et al. (2013)	H2a+152 16311
Iraq	JQ995834	Al-Zahery et al. (2013)	U3b2a1a
Iraq	JQ995835	Al-Zahery et al. (2013)	U5b2a1a2
Iraq	JQ995836	Al-Zahery et al. (2013)	HV14
Iraq	JQ995837	Al-Zahery et al. (2013)	U2d1
Iraq	JQ995838	Al-Zahery et al. (2013)	J1b9
Iraq	JQ995839	Al-Zahery et al. (2013)	U4
Iraq	JQ995840	Al-Zahery et al. (2013)	H1e1a6
Iraq	JQ995841	Al-Zahery et al. (2013)	J1d2
Iraq	JQ995842	Al-Zahery et al. (2013)	L3f1b+16292
Iraq	JQ995843	Al-Zahery et al. (2013)	U7a
Iraq	JQ995844	Al-Zahery et al. (2013)	U3
Iraq	JQ995845	Al-Zahery et al. (2013)	U4a2
Iraq	JQ995846	Al-Zahery et al. (2013)	K2
Iraq	JQ995847	Al-Zahery et al. (2013)	H5
Iraq	JQ995848	Al-Zahery et al. (2013)	H85
Iraq	JQ995849	Al-Zahery et al. (2013)	H14b1
Iraq	JQ995850	Al-Zahery et al. (2013)	I5c
Iraq	JQ995851	Al-Zahery et al. (2013)	L2a1c+16129
Iraq	JQ995852	Al-Zahery et al. (2013)	B4b1a3
Iraq	JQ995853	Al-Zahery et al. (2013)	R9
Iraq	JQ995854	Al-Zahery et al. (2013)	I1
Iraq	JQ995855	Al-Zahery et al. (2013)	H14a
Iraq	JQ995856	Al-Zahery et al. (2013)	K1a
Iraq	JQ995857	Al-Zahery et al. (2013)	L2a1+143
Iraq	JQ995858	Al-Zahery et al. (2013)	H7i
Iraq	JQ995859	Al-Zahery et al. (2013)	U3b1a1
Iraq	JQ995860	Al-Zahery et al. (2013)	H1e1a4
Iraq	JQ995861	Al-Zahery et al. (2013)	HV14
Iraq	JQ995862	Al-Zahery et al. (2013)	H5
Iraq	JQ995863	Al-Zahery et al. (2013)	K1a
Iraq	JQ995864	Al-Zahery et al. (2013)	L2a1a3
Iraq	JQ995865	Al-Zahery et al. (2013)	J1b1b

Population	GenBank	Reference	Haplogroup (HG)
Iraq	JQ995866	Al-Zahery et al. (2013)	P2
Iraq	JQ995867	Al-Zahery et al. (2013)	H33c
Iraq	JQ995868	Al-Zahery et al. (2013)	HV1b+152
Iraq	JQ995869	Al-Zahery et al. (2013)	R0a2i
Iraq	JQ995870	Al-Zahery et al. (2013)	U1a1a1
Iraq	JQ995871	Al-Zahery et al. (2013)	HV1a1
Iraq	JQ995872	Al-Zahery et al. (2013)	T2
Iraq	JQ995873	Al-Zahery et al. (2013)	H3z
Iraq	JQ995874	Al-Zahery et al. (2013)	K1a4a1a+195
Iraq	JQ995875	Al-Zahery et al. (2013)	U5a1
Iraq	JQ995876	Al-Zahery et al. (2013)	U7a1
Iraq	JQ995877	Al-Zahery et al. (2013)	H6b1
Iraq	JQ995878	Al-Zahery et al. (2013)	L3e5e
Iraq	JQ995879	Al-Zahery et al. (2013)	T2a+195
Iraq	JQ995880	Al-Zahery et al. (2013)	H7c1
Iraq	JQ995881	Al-Zahery et al. (2013)	H29
Iraq	JQ995882	Al-Zahery et al. (2013)	H10+(16093)
Iraq	JQ995883	Al-Zahery et al. (2013)	U9a
Iraq	JQ995884	Al-Zahery et al. (2013)	J1b7a
Iraq	JQ995885	Al-Zahery et al. (2013)	K1a4a1c1
Iraq	JQ995886	Al-Zahery et al. (2013)	L3i1a
Iraq	JQ995887	Al-Zahery et al. (2013)	B4c1c
Iraq	JQ995888	Al-Zahery et al. (2013)	T
Iraq	JQ995889	Al-Zahery et al. (2013)	T3
Iraq	JQ995890	Al-Zahery et al. (2013)	U1a1a
Iraq	JQ995891	Al-Zahery et al. (2013)	J1c15b
Iraq	JQ995892	Al-Zahery et al. (2013)	N1b1
Iraq	JQ995893	Al-Zahery et al. (2013)	U5a1g2
Iraq	JQ995894	Al-Zahery et al. (2013)	J2a2a1a
Iraq	JQ995895	Al-Zahery et al. (2013)	J1b8
Iraq	JQ995896	Al-Zahery et al. (2013)	U3a
Iraq	JQ995897	Al-Zahery et al. (2013)	J1d1
Iraq	JQ995898	Al-Zahery et al. (2013)	T1a+152
Iraq	JQ995899	Al-Zahery et al. (2013)	HV1
Iraq	JQ995900	Al-Zahery et al. (2013)	H1u2
Iraq	JQ995901	Al-Zahery et al. (2013)	J2a2

Population	GenBank	Reference	Haplogroup (HG)
Iraq	JQ995902	Al-Zahery et al. (2013)	U1a1a3
Iraq	JQ995903	Al-Zahery et al. (2013)	T2i1
Iraq	JQ995904	Al-Zahery et al. (2013)	U1a2
Iraq	JQ995905	Al-Zahery et al. (2013)	L3f1b+16292
Iraq	JQ995906	Al-Zahery et al. (2013)	U7a4a1
Iraq	JQ995907	Al-Zahery et al. (2013)	H57
Iraq	JQ995908	Al-Zahery et al. (2013)	T1a2b
Iraq	JQ995909	Al-Zahery et al. (2013)	B6
Iraq	JQ995910	Al-Zahery et al. (2013)	K1a8
Iraq	JQ995911	Al-Zahery et al. (2013)	H5
Iraq	JQ995912	Al-Zahery et al. (2013)	N1b1
Iraq	JQ995913	Al-Zahery et al. (2013)	T2b3+151
Iraq	JQ995914	Al-Zahery et al. (2013)	J1b
Iraq	JQ995915	Al-Zahery et al. (2013)	L0a2a2
Iraq	JQ995916	Al-Zahery et al. (2013)	H2a2a
Iraq	JQ995917	Al-Zahery et al. (2013)	L3f1b1a
Iraq	JQ995918	Al-Zahery et al. (2013)	L2a1c+16129
Iraq	JQ995919	Al-Zahery et al. (2013)	J2a2a1a
Iraq	JQ995920	Al-Zahery et al. (2013)	H2a2a
Iraq	JQ995921	Al-Zahery et al. (2013)	L3f1b+16292+150
Iraq	JQ995922	Al-Zahery et al. (2013)	HV1a1
Iraq	JQ995923	Al-Zahery et al. (2013)	L3b1a+@16124
Iraq	JQ995924	Al-Zahery et al. (2013)	W+194
Iraq	JQ995925	Al-Zahery et al. (2013)	U9a
Iraq	JQ995926	Al-Zahery et al. (2013)	H2a3
Iraq	JQ995927	Al-Zahery et al. (2013)	U3
Iraq	JQ995928	Al-Zahery et al. (2013)	J1b
Iraq	JQ995929	Al-Zahery et al. (2013)	L0a2c
Iraq	JQ995930	Al-Zahery et al. (2013)	H3x
Iraq	JQ995931	Al-Zahery et al. (2013)	X2e2b
Iraq	JQ995932	Al-Zahery et al. (2013)	H1+16355
Iraq	JQ995933	Al-Zahery et al. (2013)	H5s
Iraq	JQ995934	Al-Zahery et al. (2013)	H5n
Iraq	JQ995935	Al-Zahery et al. (2013)	U7a
Iraq	JQ995936	Al-Zahery et al. (2013)	T
Iraq	JQ995937	Al-Zahery et al. (2013)	U6a4

Population	GenBank	Reference	Haplogroup (HG)
Iraq	JQ995938	Al-Zahery et al. (2013)	I1a1
Iraq	JQ995939	Al-Zahery et al. (2013)	L1c3a1b
Iraq	JQ995940	Al-Zahery et al. (2013)	N1b1
Iraq	JQ995941	Al-Zahery et al. (2013)	H57
Iraq	JQ995942	Al-Zahery et al. (2013)	T1a1'3
Iraq	JQ995943	Al-Zahery et al. (2013)	HV4a
Iraq	JQ995944	Al-Zahery et al. (2013)	L3b
Iraq	JQ995945	Al-Zahery et al. (2013)	L2a1g
Iraq	JQ995946	Al-Zahery et al. (2013)	R0a2c
Iraq	JQ995947	Al-Zahery et al. (2013)	L3i2
Iraq	JQ995948	Al-Zahery et al. (2013)	N1b1
Iraq	JQ995949	Al-Zahery et al. (2013)	HV1b1
Iraq	JQ995950	Al-Zahery et al. (2013)	H107
Iraq	JQ995951	Al-Zahery et al. (2013)	H66a
Iraq	JQ995952	Al-Zahery et al. (2013)	H1m1
Iraq	JQ995953	Al-Zahery et al. (2013)	H1e1a6
Iraq	JQ995954	Al-Zahery et al. (2013)	X2
Iraq	JQ995955	Al-Zahery et al. (2013)	H11
Iraq	JQ995956	Al-Zahery et al. (2013)	K1a
Iraq	JQ995957	Al-Zahery et al. (2013)	U2e1b
Iraq	JQ995958	Al-Zahery et al. (2013)	H10+(16093)
Iraq	JQ995959	Al-Zahery et al. (2013)	U4a2
Iraq	JQ995960	Al-Zahery et al. (2013)	U3b3
Iraq	JQ995961	Al-Zahery et al. (2013)	HV4a2a
Iraq	JQ995962	Al-Zahery et al. (2013)	J1b3a
Iraq	JQ995963	Al-Zahery et al. (2013)	T2c1
Iraq	JQ995964	Al-Zahery et al. (2013)	H2a2a
Iraq	JQ995965	Al-Zahery et al. (2013)	HV1b+152
Iraq	JQ995966	Al-Zahery et al. (2013)	H27
Iraq	JQ995967	Al-Zahery et al. (2013)	H27
Iraq	JQ995968	Al-Zahery et al. (2013)	M1
Iraq	JQ995969	Al-Zahery et al. (2013)	J1b5a
Iraq	JQ995970	Al-Zahery et al. (2013)	W3a1+199
Iraq	JQ995971	Al-Zahery et al. (2013)	U7a
Iraq	JQ995972	Al-Zahery et al. (2013)	H5
Iraq	JQ995973	Al-Zahery et al. (2013)	J1b

Population	GenBank	Reference	Haplogroup (HG)
Iraq	JQ995974	Al-Zahery et al. (2013)	J1c
Iraq	JQ995975	Al-Zahery et al. (2013)	T1a7
Iraq	JQ995976	Al-Zahery et al. (2013)	L3e5e
Iraq	JQ995977	Al-Zahery et al. (2013)	U3c
Iraq	JQ995978	Al-Zahery et al. (2013)	U4
Iraq	JQ995979	Al-Zahery et al. (2013)	M1a1
Iraq	JQ995980	Al-Zahery et al. (2013)	H3x
Iraq	JQ995981	Al-Zahery et al. (2013)	J1b
Iraq	JQ995982	Al-Zahery et al. (2013)	U1b2
Iraq	JQ995983	Al-Zahery et al. (2013)	T1b
Iraq	JQ995984	Al-Zahery et al. (2013)	H2a2a
Israel	JQ797878	Pala et al. (2012)	J1c12
Israel	JQ797920	Pala et al. (2012)	J2a2a1a1
Israel	JQ798022	Pala et al. (2012)	T1a1
Israel	JQ798027	Pala et al. (2012)	T1a2
Israel	JQ798086	Pala et al. (2012)	T2b
Israel	JQ798096	Pala et al. (2012)	T2c1b1b
Israel	JQ798100	Pala et al. (2012)	T2c1c1
Israel	DQ301792	Behar et al. (2006)	K1a4b
Israel	DQ301793	Behar et al. (2006)	K1a5
Israel	DQ301799	Behar et al. (2006)	K1a6
Israel	DQ301801	Behar et al. (2006)	K1a6
Israel	EF060332	Olivieri et al. (2006)	M1a1e
Israel	AY738942	Achilli et al. (2004)	HV1b
Israel	JQ245761	Fernandes et al. (2012)	W6
Israel	JQ245762	Fernandes et al. (2012)	W6
Israel	JQ245763	Fernandes et al. (2012)	X2b
Jordan	JQ798038	Pala et al. (2012)	T1b1
Jordan	AM263189	Roostalu et al. (2007)	H13a2b1
Jordan	AF381996.2	Maca-Meyer et al. (2001)	M12
Jordan	AF382000	Maca-Meyer et al. (2001)	U2
Jordan	AF381999	Maca-Meyer et al. (2001)	N1b
Jordan	AF381998	Maca-Meyer et al. (2001)	L3d
Jordan	AF381997	Maca-Meyer et al. (2001)	R1
Jordan	AF381995	Maca-Meyer et al. (2001)	U21
Jordan	GQ888731	Garcia et al. (2011)	HV4a2

Population	GenBank	Reference	Haplogroup (HG)
Jordan	FJ236978	Ennafaa et al. (2009)	H5
Jordan	DQ779929	Gonzalez et al. (2007)	M1a
Jordan	DQ200805	Gonzalez et al. (2006)	U8b
Kalmyk	JN857049	Derenko et al. (2012)	M9a1b2
Kalmyk	JN857048	Derenko et al. (2012)	M9a1a1a1*
Kalmyk	JN857047	Derenko et al. (2012)	M10a2a
Kalmyk	FJ951588	Derenko et al. (2010)	D2b1
Kalmyk	KJ856729	Derenko et al. (2010)	U4a1*
Kalmyk	GU213237	Palanichamy et al. (2015)	U7
Ket	AY519486.1	Starikovskaya et al. (2005)	A8a
Ket	FJ493512	Sukernik et al. (2012)	Z1a
Ket	EU482362	Volodko et al. (2008)	D6
Ket	EU787451	Derbeneva et al. (2002a)	N2
Khamnigan	JN857046	Derenko et al. (2012)	B4c1a2a
Khamnigan	JN857045	Derenko et al. (2012)	B4b1a3a1a
Khamnigan	JN857044	Derenko et al. (2012)	B4b1a3a1a
Khamnigan	JN857043	Derenko et al. (2012)	B4b1a3a1a
Khamnigan	JN857042	Derenko et al. (2012)	N9a1
Khamnigan	JN857041	Derenko et al. (2012)	B4i
Khamnigan	JN857040	Derenko et al. (2012)	M9a1a1a1
Khamnigan	JN857039	Derenko et al. (2012)	B5b2b
Khamnigan	FJ951573	Derenko et al. (2010)	C4b4
Khamnigan	FJ951574	Derenko et al. (2010)	D4c2a
Khamnigan	FJ951575	Derenko et al. (2010)	D4q
Khamnigan	FJ951576	Derenko et al. (2010)	C5b*
Khamnigan	FJ951577	Derenko et al. (2010)	C4a1b1
Khamnigan	FJ951578	Derenko et al. (2010)	D4g2a
Khamnigan	FJ951579	Derenko et al. (2010)	C4a2a*
Khamnigan	FJ951580	Derenko et al. (2010)	C4b5
Khamnigan	FJ951581	Derenko et al. (2010)	D4b1a2
Khamnigan	FJ951582	Derenko et al. (2010)	D4j5
Khamnigan	FJ951583	Derenko et al. (2010)	C5a1
Khamnigan	FJ951584	Derenko et al. (2010)	D4j4
Kyrgyzstan	GU069689	Irwin et al. (2010)	U5a2a
Kyrgyzstan	GU069690	Irwin et al. (2010)	F2a
Kyrgyzstan	GU069691	Irwin et al. (2010)	M9

Population	GenBank	Reference	Haplogroup (HG)
Kyrgyzstan	GU069692	Irwin et al. (2010)	H1+152
Kyrgyzstan	GU069693	Irwin et al. (2010)	U4
Kyrgyzstan	GU069694	Irwin et al. (2010)	Y1
Kyrgyzstan	GU069695	Irwin et al. (2010)	X2
Kyrgyzstan	GU069696	Irwin et al. (2010)	D4c1a
Kyrgyzstan	GU069697	Irwin et al. (2010)	M9
Kyrgyzstan	GU069698	Irwin et al. (2010)	F1b1+@152
Kyrgyzstan	GU069699	Irwin et al. (2010)	C4a1a3d
Kyrgyzstan	GU069700	Irwin et al. (2010)	B4+16261
Kyrgyzstan	GU069701	Irwin et al. (2010)	C4a2c1
Kyrgyzstan	GU069702	Irwin et al. (2010)	D5a2a1+@16172
Kyrgyzstan	GU069703	Irwin et al. (2010)	H2a2a
Kyrgyzstan	GU069704	Irwin et al. (2010)	C5b1b
Kyrgyzstan	GU069705	Irwin et al. (2010)	J2b1a
Kyrgyzstan	GU069706	Irwin et al. (2010)	I1
Kyrgyzstan	GU069707	Irwin et al. (2010)	M30c1
Kyrgyzstan	GU069708	Irwin et al. (2010)	D4b2a2a
Kyrgyzstan	GU069709	Irwin et al. (2010)	M7b1a1c
Kyrgyzstan	GU069710	Irwin et al. (2010)	C
Kyrgyzstan	GU069711	Irwin et al. (2010)	H3v
Kyrgyzstan	GU069712	Irwin et al. (2010)	B4h1
Kyrgyzstan	GU069713	Irwin et al. (2010)	D5
Kyrgyzstan	GU069714	Irwin et al. (2010)	C
Kyrgyzstan	GU069715	Irwin et al. (2010)	D5b1a1
Kyrgyzstan	GU069716	Irwin et al. (2010)	T1
Kyrgyzstan	GU069717	Irwin et al. (2010)	B4h
Kyrgyzstan	GU069718	Irwin et al. (2010)	A8a
Kyrgyzstan	GU069719	Irwin et al. (2010)	D5a2a1
Kyrgyzstan	GU069720	Irwin et al. (2010)	G2a+152
Kyrgyzstan	GU069721	Irwin et al. (2010)	M10a1+16129
Kyrgyzstan	GU069722	Irwin et al. (2010)	A+152+16362
Kyrgyzstan	GU069723	Irwin et al. (2010)	B4+16261
Kyrgyzstan	GU069724	Irwin et al. (2010)	D4e2a
Kyrgyzstan	GU069725	Irwin et al. (2010)	C
Kyrgyzstan	GU069726	Irwin et al. (2010)	D4g2a
Kyrgyzstan	GU069727	Irwin et al. (2010)	I

Population	GenBank	Reference	Haplogroup (HG)
Kyrgyzstan	GU069728	Irwin et al. (2010)	D4g2a
Kyrgyzstan	GU069729	Irwin et al. (2010)	B4c1b2b
Kyrgyzstan	GU069730	Irwin et al. (2010)	D4j+146
Kyrgyzstan	GU069731	Irwin et al. (2010)	H11a2
Kyrgyzstan	GU069732	Irwin et al. (2010)	F1b1+@152
Kyrgyzstan	GU069733	Irwin et al. (2010)	W1e1
Kyrgyzstan	GU069734	Irwin et al. (2010)	U5a1b1
Kyrgyzstan	GU069735	Irwin et al. (2010)	C
Kyrgyzstan	GU069736	Irwin et al. (2010)	A+152+16362+16189
Kyrgyzstan	GU069737	Irwin et al. (2010)	D4j3
Kyrgyzstan	GU069738	Irwin et al. (2010)	C4a2
Kyrgyzstan	GU069739	Irwin et al. (2010)	U4a1
Kyrgyzstan	GU069740	Irwin et al. (2010)	B4h1
Kyrgyzstan	GU069741	Irwin et al. (2010)	C4a1a+195
Kyrgyzstan	GU069742	Irwin et al. (2010)	U8a
Kyrgyzstan	GU069743	Irwin et al. (2010)	M13'46'61+16362
Kyrgyzstan	GU069744	Irwin et al. (2010)	D4b1
Kyrgyzstan	GU069745	Irwin et al. (2010)	K1c1e
Kyrgyzstan	GU069746	Irwin et al. (2010)	D4a3
Kyrgyzstan	GU069747	Irwin et al. (2010)	M43a1
Kyrgyzstan	GU069748	Irwin et al. (2010)	U4b1b1b
Kyrgyzstan	GU069749	Irwin et al. (2010)	W6
Kyrgyzstan	GU069750	Irwin et al. (2010)	I1
Kyrgyzstan	GU069751	Irwin et al. (2010)	M5a2a1a2
Kyrgyzstan	GU069752	Irwin et al. (2010)	B4c2
Kyrgyzstan	GU069753	Irwin et al. (2010)	D4c2a
Kyrgyzstan	GU069754	Irwin et al. (2010)	D4b2b
Kyrgyzstan	GU069755	Irwin et al. (2010)	U4b1a1a1
Kyrgyzstan	GU069756	Irwin et al. (2010)	M5a2a1a2
Kyrgyzstan	GU069757	Irwin et al. (2010)	M3a1+204
Kyrgyzstan	GU069758	Irwin et al. (2010)	U7a
Kyrgyzstan	GU069759	Irwin et al. (2010)	U4
Kyrgyzstan	GU069760	Irwin et al. (2010)	C4a1b
Kyrgyzstan	GU069761	Irwin et al. (2010)	M9
Kyrgyzstan	GU069762	Irwin et al. (2010)	B4h
Kyrgyzstan	GU069763	Irwin et al. (2010)	HV1a1

Population	GenBank	Reference	Haplogroup (HG)
Kyrgyzstan	GU069764	Irwin et al. (2010)	W6
Kyrgyzstan	GU069765	Irwin et al. (2010)	H3v
Kyrgyzstan	GU069766	Irwin et al. (2010)	D4b2b
Kyrgyzstan	GU069767	Irwin et al. (2010)	H7h
Kyrgyzstan	GU069768	Irwin et al. (2010)	D4+195
Kyrgyzstan	GU069769	Irwin et al. (2010)	C4a2c1
Kyrgyzstan	GU069770	Irwin et al. (2010)	N9a1'3
Kyrgyzstan	GU069771	Irwin et al. (2010)	M7b1a2a
Kyrgyzstan	GU069772	Irwin et al. (2010)	K1a
Kyrgyzstan	GU069773	Irwin et al. (2010)	U4a1
Kyrgyzstan	GU069774	Irwin et al. (2010)	C
Kyrgyzstan	GU069775	Irwin et al. (2010)	G2a2a
Kyrgyzstan	GU069776	Irwin et al. (2010)	N9a1
Kyrgyzstan	GU069777	Irwin et al. (2010)	B4+16261
Kyrgyzstan	GU069778	Irwin et al. (2010)	C4a1a+195
Kyrgyzstan	GU069779	Irwin et al. (2010)	U2b
Kyrgyzstan	GU069780	Irwin et al. (2010)	G2a+152
Kyrgyzstan	GU069781	Irwin et al. (2010)	D4b2b
Kyrgyzstan	GU069782	Irwin et al. (2010)	U5b2a1a
Kyrgyzstan	GU069783	Irwin et al. (2010)	M
Kyrgyzstan	GU069784	Irwin et al. (2010)	M65a+@16311
Kyrgyzstan	GU069785	Irwin et al. (2010)	H15
Kyrgyzstan	GU069786	Irwin et al. (2010)	H11
Kyrgyzstan	GU069787	Irwin et al. (2010)	M66b
Kyrgyzstan	GU069788	Irwin et al. (2010)	B4c1b2b
Kyrgyzstan	GU069789	Irwin et al. (2010)	W1e1
Kyrgyzstan	GU069790	Irwin et al. (2010)	B4b1a3
Kyrgyzstan	GU069791	Irwin et al. (2010)	H2a+152 16311
Kyrgyzstan	GU069792	Irwin et al. (2010)	D4c2b
Kyrgyzstan	GU069793	Irwin et al. (2010)	C
Kyrgyzstan	GU069794	Irwin et al. (2010)	B4c1b2b
Kyrgyzstan	GU069795	Irwin et al. (2010)	T1a
Kyrgyzstan	GU069796	Irwin et al. (2010)	C
Kyrgyzstan	GU069797	Irwin et al. (2010)	H1m1
Kyrgyzstan	GU069798	Irwin et al. (2010)	HV14
Kyrgyzstan	GU069799	Irwin et al. (2010)	M5a2a1a2

Population	GenBank	Reference	Haplogroup (HG)
Kyrgyzstan	GU069800	Irwin et al. (2010)	B4h1
Kyrgyzstan	GU069801	Irwin et al. (2010)	J1b1a1+146
Kyrgyzstan	GU069802	Irwin et al. (2010)	M18a
Kyrgyzstan	GU069803	Irwin et al. (2010)	U5a1
Kyrgyzstan	GU069804	Irwin et al. (2010)	U3b1a1
Kyrgyzstan	GU069805	Irwin et al. (2010)	A+152+16362
Kyrgyzstan	GU069806	Irwin et al. (2010)	D4c2a
Kyrgyzstan	GU069807	Irwin et al. (2010)	F1b1b
Kyrgyzstan	GU069808	Irwin et al. (2010)	U2e1
Kyrgyzstan	GU069809	Irwin et al. (2010)	M9
Kyrgyzstan	GU069810	Irwin et al. (2010)	M33a2'3
Kyrgyzstan	GU069811	Irwin et al. (2010)	U4b1b1b
Kyrgyzstan	GU069812	Irwin et al. (2010)	M13a1b
Kyrgyzstan	GU069813	Irwin et al. (2010)	M9
Kyrgyzstan	GU069814	Irwin et al. (2010)	M5a2a1a2
Kyrgyzstan	GU069815	Irwin et al. (2010)	T2d1
Kyrgyzstan	GU069816	Irwin et al. (2010)	D4I2
Kyrgyzstan	GU069817	Irwin et al. (2010)	U4a1
Kyrgyzstan	GU069818	Irwin et al. (2010)	M7b1a2a
Kyrgyzstan	GU069819	Irwin et al. (2010)	D5a2a1
Kyrgyzstan	GU069820	Irwin et al. (2010)	Y1
Kyrgyzstan	GU069821	Irwin et al. (2010)	U5b2a1a
Kyrgyzstan	GU069822	Irwin et al. (2010)	F1b1+@152
Kyrgyzstan	GU069823	Irwin et al. (2010)	B4a1c3
Kyrgyzstan	GU069824	Irwin et al. (2010)	D4i
Kyrgyzstan	GU069825	Irwin et al. (2010)	B4a1c3
Kyrgyzstan	GU069826	Irwin et al. (2010)	H1n+146+195
Kyrgyzstan	GU069827	Irwin et al. (2010)	A8a
Kyrgyzstan	GU069828	Irwin et al. (2010)	M8a3a
Kyrgyzstan	GU069829	Irwin et al. (2010)	T1
Kyrgyzstan	GU069830	Irwin et al. (2010)	R2
Kyrgyzstan	GU069831	Irwin et al. (2010)	N11a1
Kyrgyzstan	GU069832	Irwin et al. (2010)	D4c2b
Kyrgyzstan	GU069833	Irwin et al. (2010)	M9
Kyrgyzstan	GU069834	Irwin et al. (2010)	D5c1a
Kyrgyzstan	GU069835	Irwin et al. (2010)	D5a2a+16092

Population	GenBank	Reference	Haplogroup (HG)
Kyrgyzstan	GU069836	Irwin et al. (2010)	Z+152
Kyrgyzstan	GU069837	Irwin et al. (2010)	D4b2d
Kyrgyzstan	GU069838	Irwin et al. (2010)	A8a
Kyrgyzstan	GU069839	Irwin et al. (2010)	C5a
Kyrgyzstan	GU069840	Irwin et al. (2010)	U5b2a1a2
Kyrgyzstan	GU069841	Irwin et al. (2010)	G2a+152
Kyrgyzstan	GU069842	Irwin et al. (2010)	C4a2c1
Kyrgyzstan	GU069843	Irwin et al. (2010)	Z4a
Kyrgyzstan	GU069844	Irwin et al. (2010)	D4c2a
Kyrgyzstan	GU069845	Irwin et al. (2010)	U5a1b1
Kyrgyzstan	GU069846	Irwin et al. (2010)	J1b1a1+146
Kyrgyzstan	GU069847	Irwin et al. (2010)	G2a
Kyrgyzstan	GU069848	Irwin et al. (2010)	V+@72
Kyrgyzstan	GU069849	Irwin et al. (2010)	C4b1
Kyrgyzstan	GU069850	Irwin et al. (2010)	M9
Kyrgyzstan	GU069851	Irwin et al. (2010)	D4j3
Kyrgyzstan	GU069852	Irwin et al. (2010)	A+152+16362+200
Kyrgyzstan	GU069853	Irwin et al. (2010)	C4b2
Kyrgyzstan	GU069854	Irwin et al. (2010)	D4i
Kyrgyzstan	GU069855	Irwin et al. (2010)	B4c1b2b
Kyrgyzstan	GU069856	Irwin et al. (2010)	B4b1a3
Kyrgyzstan	GU069857	Irwin et al. (2010)	D4o2a
Kyrgyzstan	GU069858	Irwin et al. (2010)	D4a3
Kyrgyzstan	GU069859	Irwin et al. (2010)	M9
Kyrgyzstan	GU069860	Irwin et al. (2010)	J2b
Kyrgyzstan	GU069861	Irwin et al. (2010)	M9
Kyrgyzstan	GU069862	Irwin et al. (2010)	D5b
Kyrgyzstan	GU069863	Irwin et al. (2010)	B5b
Kyrgyzstan	GU069864	Irwin et al. (2010)	C5a
Kyrgyzstan	GU069865	Irwin et al. (2010)	Y1
Kyrgyzstan	GU069866	Irwin et al. (2010)	H5
Kyrgyzstan	GU069867	Irwin et al. (2010)	D5b
Kyrgyzstan	GU069868	Irwin et al. (2010)	M7b1a1a1
Kyrgyzstan	GU069869	Irwin et al. (2010)	D4b1a2a1
Kyrgyzstan	GU069870	Irwin et al. (2010)	D4j3
Kyrgyzstan	GU069871	Irwin et al. (2010)	B4b1b

Population	GenBank	Reference	Haplogroup (HG)
Kyrgyzstan	GU069872	Irwin et al. (2010)	H7h
Kyrgyzstan	GU069873	Irwin et al. (2010)	T1
Kyrgyzstan	GU069874	Irwin et al. (2010)	T1
Kyrgyzstan	GU069875	Irwin et al. (2010)	U5b2a1a
Kyrgyzstan	GU069876	Irwin et al. (2010)	C5a
Kyrgyzstan	GU069877	Irwin et al. (2010)	A8a
Kyrgyzstan	GU069878	Irwin et al. (2010)	C5b1
Kyrgyzstan	GU069879	Irwin et al. (2010)	HV1a1
Kyrgyzstan	GU069880	Irwin et al. (2010)	C4a2c
Kyrgyzstan	GU069881	Irwin et al. (2010)	C4a1a+195
Kyrgyzstan	GU069882	Irwin et al. (2010)	A14
Kyrgyzstan	GU069883	Irwin et al. (2010)	C4+152
Kyrgyzstan	GU069884	Irwin et al. (2010)	H1b
Kyrgyzstan	GU069885	Irwin et al. (2010)	D4j+(16286)
Kyrgyzstan	GU069886	Irwin et al. (2010)	M64
Kyrgyzstan	GU069887	Irwin et al. (2010)	A24
Kyrgyzstan	GU069888	Irwin et al. (2010)	M10a1+16129
Kyrgyzstan	GU069889	Irwin et al. (2010)	M9
Kyrgyzstan	GU069890	Irwin et al. (2010)	M9
Kyrgyzstan	GU069891	Irwin et al. (2010)	D4b1a2a1
Kyrgyzstan	GU069892	Irwin et al. (2010)	A12a
Kyrgyzstan	GU069893	Irwin et al. (2010)	C5a2b
Kyrgyzstan	GU069894	Irwin et al. (2010)	H2a2a
Kyrgyzstan	GU069895	Irwin et al. (2010)	U5a2a
Kyrgyzstan	GU069896	Irwin et al. (2010)	D4b2b
Kyrgyzstan	GU069897	Irwin et al. (2010)	H11
Kyrgyzstan	GU069898	Irwin et al. (2010)	N1b1
Kyrgyzstan	GU069899	Irwin et al. (2010)	D4c2a
Kyrgyzstan	GU069900	Irwin et al. (2010)	U4'9
Kyrgyzstan	GU069901	Irwin et al. (2010)	B4h
Kyrgyzstan	GU069902	Irwin et al. (2010)	B4+16261
Kyrgyzstan	GU069903	Irwin et al. (2010)	C4+152+16093
Kyrgyzstan	GU069904	Irwin et al. (2010)	Y1
Kyrgyzstan	GU069905	Irwin et al. (2010)	G1a1
Kyrgyzstan	GU069906	Irwin et al. (2010)	C4a1a3d
Kyrgyzstan	GU069907	Irwin et al. (2010)	C4a1a+195

Population	GenBank	Reference	Haplogroup (HG)
Kyrgyzstan	GU069908	Irwin et al. (2010)	C5b1
Kyrgyzstan	GU069909	Irwin et al. (2010)	H2a2a
Kyrgyzstan	GU069910	Irwin et al. (2010)	U3a
Kyrgyzstan	GU069911	Irwin et al. (2010)	C4a1a4a
Kyrgyzstan	GU069912	Irwin et al. (2010)	A12a
Kyrgyzstan	GU069913	Irwin et al. (2010)	J1b1a1+146
Kyrgyzstan	GU069914	Irwin et al. (2010)	M8a2a1
Kyrgyzstan	GU069915	Irwin et al. (2010)	D4j3
Kyrgyzstan	GU069916	Irwin et al. (2010)	J1b1a1+146
Kyrgyzstan	GU069917	Irwin et al. (2010)	J1b1a1
Kyrgyzstan	GU069918	Irwin et al. (2010)	Y
Kyrgyzstan	GU069919	Irwin et al. (2010)	M5a2a1a2
Kyrgyzstan	GU069920	Irwin et al. (2010)	G2a2a
Kyrgyzstan	GU069921	Irwin et al. (2010)	D4i
Kyrgyzstan	GU069922	Irwin et al. (2010)	D5a2a+16092
Kyrgyzstan	GU069923	Irwin et al. (2010)	C4b1
Kyrgyzstan	GU069924	Irwin et al. (2010)	F2b1
Kyrgyzstan	GU069925	Irwin et al. (2010)	H1e1a1
Kyrgyzstan	GU069926	Irwin et al. (2010)	A+152+16362+16189
Kyrgyzstan	GU069927	Irwin et al. (2010)	G2a5
Kyrgyzstan	GU069928	Irwin et al. (2010)	D4a3
Kyrgyzstan	GU069929	Irwin et al. (2010)	M43a1
Kyrgyzstan	GU069930	Irwin et al. (2010)	N9a1'3
Kyrgyzstan	GU069931	Irwin et al. (2010)	M37+152+151
Kyrgyzstan	GU069932	Irwin et al. (2010)	A+152+16362+16189
Kyrgyzstan	GU069933	Irwin et al. (2010)	Y1
Kyrgyzstan	GU069934	Irwin et al. (2010)	Z+152
Kyrgyzstan	GU069935	Irwin et al. (2010)	D4j1a
Kyrgyzstan	GU069936	Irwin et al. (2010)	H1b
Kyrgyzstan	GU069937	Irwin et al. (2010)	U4
Koryak	FJ951595	Derenko et al. (2010)	C5a2a
Koryak	FJ951596	Derenko et al. (2010)	C5a2a
Koryak	FJ951597	Derenko et al. (2010)	C5a2a
Koryak	FJ951598	Derenko et al. (2010)	C4b2
Koryak	FJ951599	Derenko et al. (2010)	C5a2a
Koryak	EF153825	Derenko et al. (2007)	Y1

Population	GenBank	Reference	Haplogroup (HG)
Koryak	EF153826	Derenko et al. (2007)	G1b
Koryak	EF153827	Derenko et al. (2007)	A2b
Koryak	EF153828	Derenko et al. (2007)	G1b
Koryak	EF153829	Derenko et al. (2007)	G1b
Koryak	EF153830	Derenko et al. (2007)	G1b
Koryak	EU007851	Ingman and Gyllensten (2007)	U5a2a1
Koryak	EU007850	Ingman and Gyllensten (2007)	C5a2b1
Koryak	EU007849	Ingman and Gyllensten (2007)	G1b+16129
Koryak	EU007848	Ingman and Gyllensten (2007)	Y1a2
Koryak	AY519487.2	Starikovskaya et al. (2005)	C4b2a
Koryak	AY195762.2	Mishmar et al. (2003)	M5
Koryak	AY195763.2	Mishmar et al. (2003)	C4b2a
Koryak	AY195761	Mishmar et al. (2003)	Z1a
Kuwait	HQ679958	Scheible et al. (2011)	J2a2b
Kuwait	HQ679959	Scheible et al. (2011)	U1a2
Kuwait	HQ679960	Scheible et al. (2011)	T1a
Kuwait	HQ679961	Scheible et al. (2011)	N1a3a
Kuwait	HQ679962	Scheible et al. (2011)	J2a2
Kuwait	HQ679963	Scheible et al. (2011)	J1b
Kuwait	HQ679964	Scheible et al. (2011)	H57
Kuwait	HQ679965	Scheible et al. (2011)	U3b3
Kuwait	HQ679966	Scheible et al. (2011)	R0a2c
Kuwait	HQ679967	Scheible et al. (2011)	J1b
Kuwait	HQ679968	Scheible et al. (2011)	J1b1a
Kuwait	HQ679969	Scheible et al. (2011)	U9a
Kuwait	HQ679970	Scheible et al. (2011)	B4b1a+207
Kuwait	HQ679971	Scheible et al. (2011)	J1b
Kuwait	HQ679972	Scheible et al. (2011)	N1a3a
Kuwait	HQ679973	Scheible et al. (2011)	H29
Kuwait	HQ679974	Scheible et al. (2011)	K1a4c
Kuwait	HQ679975	Scheible et al. (2011)	U7a
Kuwait	HQ679976	Scheible et al. (2011)	R0a1a
Kuwait	HQ679977	Scheible et al. (2011)	J1b8
Kuwait	HQ679978	Scheible et al. (2011)	H1+16355
Kuwait	HQ679979	Scheible et al. (2011)	L2a1+143+@16309
Kuwait	HQ679980	Scheible et al. (2011)	R0a2i

Population	GenBank	Reference	Haplogroup (HG)
Kuwait	HQ679981	Scheible et al. (2011)	U1a1b
Kuwait	HQ679982	Scheible et al. (2011)	R0a2c
Kuwait	HQ679983	Scheible et al. (2011)	N1a3a
Kuwait	HQ679984	Scheible et al. (2011)	H1ba
Kuwait	HQ679985	Scheible et al. (2011)	L2a1a3c
Kuwait	HQ679986	Scheible et al. (2011)	N1a3a
Kuwait	HQ679987	Scheible et al. (2011)	L2a1c+16086
Kuwait	HQ679988	Scheible et al. (2011)	J2a2a1a
Kuwait	HQ679989	Scheible et al. (2011)	H6
Kuwait	HQ679990	Scheible et al. (2011)	R0a2c
Kuwait	HQ679991	Scheible et al. (2011)	N3
Kuwait	HQ679992	Scheible et al. (2011)	N1b1
Kuwait	HQ679993	Scheible et al. (2011)	HV1b1
Kuwait	HQ679994	Scheible et al. (2011)	K1a4c
Kuwait	HQ679995	Scheible et al. (2011)	E1a1a1
Kuwait	HQ679996	Scheible et al. (2011)	L0a2
Kuwait	HQ679997	Scheible et al. (2011)	U3a
Kuwait	HQ679998	Scheible et al. (2011)	H1aj1
Kuwait	HQ679999	Scheible et al. (2011)	M1a1
Kuwait	HQ680000	Scheible et al. (2011)	U1b2
Kuwait	HQ680001	Scheible et al. (2011)	H6b
Kuwait	HQ680002	Scheible et al. (2011)	L4a1
Kuwait	HQ680003	Scheible et al. (2011)	M30
Kuwait	HQ680004	Scheible et al. (2011)	H5n
Kuwait	HQ680005	Scheible et al. (2011)	K1a+150
Kuwait	HQ680006	Scheible et al. (2011)	R0a1a
Kuwait	HQ680007	Scheible et al. (2011)	R2
Kuwait	HQ680008	Scheible et al. (2011)	N1b1
Kuwait	HQ680009	Scheible et al. (2011)	H1aj1
Kuwait	HQ680010	Scheible et al. (2011)	R0a+60. 1T
Kuwait	HQ680011	Scheible et al. (2011)	R0a2n
Kuwait	HQ680012	Scheible et al. (2011)	T2b
Kuwait	HQ680013	Scheible et al. (2011)	J2a2a1a
Kuwait	HQ680014	Scheible et al. (2011)	H22
Kuwait	HQ680015	Scheible et al. (2011)	H1+152
Kuwait	HQ680016	Scheible et al. (2011)	J1b8

Population	GenBank	Reference	Haplogroup (HG)
Kuwait	HQ680017	Scheible et al. (2011)	N1a3a
Kuwait	HQ680018	Scheible et al. (2011)	U2b2
Kuwait	HQ680019	Scheible et al. (2011)	H2a2a
Kuwait	HQ680020	Scheible et al. (2011)	H1m1
Kuwait	HQ680021	Scheible et al. (2011)	L2a1+143+@16309
Kuwait	HQ680022	Scheible et al. (2011)	J1b8
Kuwait	HQ680023	Scheible et al. (2011)	H2a+152 16311
Kuwait	HQ680024	Scheible et al. (2011)	H2a2a
Kuwait	HQ680025	Scheible et al. (2011)	J1b8
Kuwait	HQ680026	Scheible et al. (2011)	H1f+16093
Kuwait	HQ680027	Scheible et al. (2011)	H1+16189
Kuwait	HQ680028	Scheible et al. (2011)	M3a1+204
Kuwait	HQ680029	Scheible et al. (2011)	T1a
Kuwait	HQ680030	Scheible et al. (2011)	K1a
Kuwait	HQ680031	Scheible et al. (2011)	U3b3
Kuwait	HQ680032	Scheible et al. (2011)	J1b3
Kuwait	HQ680033	Scheible et al. (2011)	U4
Kuwait	HQ680034	Scheible et al. (2011)	H42a
Kuwait	HQ680035	Scheible et al. (2011)	H107
Kuwait	HQ680036	Scheible et al. (2011)	L2a1b1a
Kuwait	HQ680037	Scheible et al. (2011)	M41
Kuwait	HQ680038	Scheible et al. (2011)	L2a1b1a
Kuwait	HQ680039	Scheible et al. (2011)	U4a2
Kuwait	HQ680040	Scheible et al. (2011)	L2a2'3
Kuwait	HQ680041	Scheible et al. (2011)	H57
Kuwait	HQ680042	Scheible et al. (2011)	R0a1a
Kuwait	HQ680043	Scheible et al. (2011)	R0a2n
Kuwait	HQ680044	Scheible et al. (2011)	R0a1a
Kuwait	HQ680045	Scheible et al. (2011)	U5a1
Kuwait	HQ680046	Scheible et al. (2011)	U7a
Kuwait	HQ680047	Scheible et al. (2011)	R0a2c
Kuwait	HQ680048	Scheible et al. (2011)	U1a2
Kuwait	HQ680049	Scheible et al. (2011)	H1an2
Kuwait	HQ680050	Scheible et al. (2011)	L5a1
Kuwait	HQ680051	Scheible et al. (2011)	H57
Kuwait	HQ680052	Scheible et al. (2011)	H14a

Population	GenBank	Reference	Haplogroup (HG)
Kuwait	HQ680053	Scheible et al. (2011)	N1a3a
Kuwait	HQ680054	Scheible et al. (2011)	T2c1d+152
Kuwait	HQ680055	Scheible et al. (2011)	R0a
Kuwait	HQ680056	Scheible et al. (2011)	J1b
Kuwait	HQ680057	Scheible et al. (2011)	J2a2a1a
Kuwait	HQ680058	Scheible et al. (2011)	L3d1a1a
Kuwait	HQ680059	Scheible et al. (2011)	H14a
Kuwait	HQ680060	Scheible et al. (2011)	J1b
Kuwait	HQ680061	Scheible et al. (2011)	R0a1a
Kuwait	HQ680062	Scheible et al. (2011)	H57
Kuwait	HQ680063	Scheible et al. (2011)	R0a1a
Kuwait	HQ680064	Scheible et al. (2011)	N1a3a
Kuwait	HQ680065	Scheible et al. (2011)	H5
Kuwait	HQ680066	Scheible et al. (2011)	R0a
Kuwait	HQ680067	Scheible et al. (2011)	U7a
Kuwait	HQ680068	Scheible et al. (2011)	H1e2c
Kuwait	HQ680069	Scheible et al. (2011)	X2
Kuwait	HQ680070	Scheible et al. (2011)	H1q3
Kuwait	HQ680071	Scheible et al. (2011)	L0a2a2
Kuwait	HQ680072	Scheible et al. (2011)	L2b
Kuwait	HQ680073	Scheible et al. (2011)	L4a1
Kuwait	HQ680074	Scheible et al. (2011)	H57
Kuwait	HQ680075	Scheible et al. (2011)	HV1
Kuwait	HQ680076	Scheible et al. (2011)	M1a1
Kuwait	HQ680077	Scheible et al. (2011)	J1b8
Kuwait	HQ680078	Scheible et al. (2011)	X2b+226
Kuwait	HQ680079	Scheible et al. (2011)	H6b1
Kuwait	HQ680080	Scheible et al. (2011)	R0a2c
Kuwait	HQ680081	Scheible et al. (2011)	U3b3
Kuwait	HQ680082	Scheible et al. (2011)	T2c1+146
Kuwait	HQ680083	Scheible et al. (2011)	J1b8
Kuwait	HQ680084	Scheible et al. (2011)	J1b
Kuwait	HQ680085	Scheible et al. (2011)	H1e1a6
Kuwait	HQ680086	Scheible et al. (2011)	B4b1a+207
Kuwait	HQ680087	Scheible et al. (2011)	X2
Kuwait	HQ680088	Scheible et al. (2011)	J2a2a1+16311

Population	GenBank	Reference	Haplogroup (HG)
Kuwait	HQ680089	Scheible et al. (2011)	T2f1
Kuwait	HQ680090	Scheible et al. (2011)	M
Kuwait	HQ680091	Scheible et al. (2011)	U4
Kuwait	HQ680092	Scheible et al. (2011)	C4+152
Kuwait	HQ680093	Scheible et al. (2011)	N1a1a
Kuwait	HQ680094	Scheible et al. (2011)	N1a3a
Kuwait	HQ680095	Scheible et al. (2011)	H101
Kuwait	HQ680096	Scheible et al. (2011)	J1b7
Kuwait	HQ680097	Scheible et al. (2011)	U1a1a+16129
Kuwait	HQ680098	Scheible et al. (2011)	U7a
Kuwait	HQ680099	Scheible et al. (2011)	HV19
Kuwait	HQ680100	Scheible et al. (2011)	J1b8
Kuwait	HQ680101	Scheible et al. (2011)	T2c1+146
Kuwait	HQ680102	Scheible et al. (2011)	L2a1d1
Kuwait	HQ680103	Scheible et al. (2011)	L2a2'3
Kuwait	HQ680104	Scheible et al. (2011)	L2a1b1a
Kuwait	HQ680105	Scheible et al. (2011)	U4
Kuwait	HQ680106	Scheible et al. (2011)	U7a4
Kuwait	HQ680107	Scheible et al. (2011)	T1a
Kuwait	HQ680108	Scheible et al. (2011)	N3
Kuwait	HQ680109	Scheible et al. (2011)	H5
Kuwait	HQ680110	Scheible et al. (2011)	M49
Kuwait	HQ680111	Scheible et al. (2011)	T1a8a
Kuwait	HQ680112	Scheible et al. (2011)	U2e1
Kuwait	HQ680113	Scheible et al. (2011)	J1b7
Kuwait	HQ680114	Scheible et al. (2011)	J1b8
Kuwait	HQ680115	Scheible et al. (2011)	M6a1b
Kuwait	HQ680116	Scheible et al. (2011)	T1a+152
Kuwait	HQ680117	Scheible et al. (2011)	H14a
Kuwait	HQ680118	Scheible et al. (2011)	J1b1b
Kuwait	HQ680119	Scheible et al. (2011)	N1b1
Kuwait	HQ680120	Scheible et al. (2011)	L3i1a
Kuwait	HQ680121	Scheible et al. (2011)	J1d1a
Kuwait	HQ680122	Scheible et al. (2011)	X2b+226
Kuwait	HQ680123	Scheible et al. (2011)	U8b1b
Kuwait	HQ680124	Scheible et al. (2011)	M1a1a1

Population	GenBank	Reference	Haplogroup (HG)
Kuwait	HQ680125	Scheible et al. (2011)	U9a
Kuwait	HQ680126	Scheible et al. (2011)	H3ak
Kuwait	HQ680127	Scheible et al. (2011)	M3
Kuwait	HQ680128	Scheible et al. (2011)	K1a
Kuwait	HQ680129	Scheible et al. (2011)	N3
Kuwait	HQ680130	Scheible et al. (2011)	U8b1a1
Kuwait	HQ680131	Scheible et al. (2011)	J1c
Kuwait	HQ680132	Scheible et al. (2011)	H3x
Kuwait	HQ680133	Scheible et al. (2011)	C4+152
Kuwait	HQ680134	Scheible et al. (2011)	R0a2c
Kuwait	HQ680135	Scheible et al. (2011)	J1b
Kuwait	HQ680136	Scheible et al. (2011)	U5a1+@16192
Kuwait	HQ680137	Scheible et al. (2011)	U7a4a1
Kuwait	HQ680138	Scheible et al. (2011)	H1e1a6
Kuwait	HQ680139	Scheible et al. (2011)	U7a
Kuwait	HQ680140	Scheible et al. (2011)	R0a1b
Kuwait	HQ680141	Scheible et al. (2011)	H57
Kuwait	HQ680142	Scheible et al. (2011)	K1a27
Kuwait	HQ680143	Scheible et al. (2011)	J1d1a
Kuwait	HQ680144	Scheible et al. (2011)	T2c1d+152
Kuwait	HQ680145	Scheible et al. (2011)	R0a1a
Kuwait	HQ680146	Scheible et al. (2011)	J1d1a
Kuwait	HQ680147	Scheible et al. (2011)	JT
Kuwait	HQ680148	Scheible et al. (2011)	R0a1a
Kuwait	HQ680149	Scheible et al. (2011)	H2a2a
Kuwait	HQ680150	Scheible et al. (2011)	R8
Kuwait	HQ680151	Scheible et al. (2011)	J2a1a1e
Kuwait	HQ680152	Scheible et al. (2011)	A8a1
Kuwait	HQ680153	Scheible et al. (2011)	J1b8
Kuwait	HQ680154	Scheible et al. (2011)	U3
Kuwait	HQ680155	Scheible et al. (2011)	J1+16193
Kuwait	HQ680156	Scheible et al. (2011)	X2+225
Kuwait	HQ680157	Scheible et al. (2011)	J2a2a1a
Kuwait	HQ680158	Scheible et al. (2011)	J2a2a1a
Kuwait	HQ680159	Scheible et al. (2011)	J2a2a1a
Kuwait	HQ680160	Scheible et al. (2011)	H57

Population	GenBank	Reference	Haplogroup (HG)
Kuwait	HQ680161	Scheible et al. (2011)	H2a2a
Kuwait	HQ680162	Scheible et al. (2011)	R0a1a
Kuwait	HQ680163	Scheible et al. (2011)	L1b
Kuwait	HQ680164	Scheible et al. (2011)	W6
Kuwait	HQ680165	Scheible et al. (2011)	L2b
Kuwait	HQ680166	Scheible et al. (2011)	H15a1a1
Kuwait	HQ680167	Scheible et al. (2011)	H1+152
Kuwait	HQ680168	Scheible et al. (2011)	N1a3a
Kuwait	HQ680169	Scheible et al. (2011)	R2
Kuwait	HQ680170	Scheible et al. (2011)	J1d1a
Kuwait	HQ680171	Scheible et al. (2011)	M2b
Kuwait	HQ680172	Scheible et al. (2011)	J1b
Kuwait	HQ680173	Scheible et al. (2011)	J1d1a
Kuwait	HQ680174	Scheible et al. (2011)	T1a1'3
Kuwait	HQ680175	Scheible et al. (2011)	H6b2
Kuwait	HQ680176	Scheible et al. (2011)	M1a1
Kuwait	HQ680177	Scheible et al. (2011)	U5a1
Kuwait	HQ680178	Scheible et al. (2011)	L2a1b1a
Kuwait	HQ680179	Scheible et al. (2011)	H101
Kuwait	HQ680180	Scheible et al. (2011)	J1b1b1c
Kuwait	HQ680181	Scheible et al. (2011)	J1+16193
Kuwait	HQ680182	Scheible et al. (2011)	H1ag1a
Kuwait	HQ680183	Scheible et al. (2011)	W3a1+199
Kuwait	HQ680184	Scheible et al. (2011)	H57
Kuwait	HQ680185	Scheible et al. (2011)	I
Kuwait	HQ680186	Scheible et al. (2011)	H1e2c
Kuwait	HQ680187	Scheible et al. (2011)	U7
Kuwait	HQ680188	Scheible et al. (2011)	J1b8
Kuwait	HQ680189	Scheible et al. (2011)	L3b2a
Kuwait	HQ680190	Scheible et al. (2011)	U1a1a
Kuwait	HQ680191	Scheible et al. (2011)	N1a3a
Kuwait	HQ680192	Scheible et al. (2011)	L2a1c1
Kuwait	HQ680193	Scheible et al. (2011)	J1c3+189
Kuwait	HQ680194	Scheible et al. (2011)	N1a3a
Kuwait	HQ680195	Scheible et al. (2011)	H1b
Kuwait	HQ680196	Scheible et al. (2011)	I7

Population	GenBank	Reference	Haplogroup (HG)
Kuwait	HQ680197	Scheible et al. (2011)	T1a+152
Kuwait	HQ680198	Scheible et al. (2011)	H57
Kuwait	HQ680199	Scheible et al. (2011)	N1b1
Kuwait	HQ680200	Scheible et al. (2011)	U9a
Kuwait	HQ680201	Scheible et al. (2011)	J2b
Kuwait	HQ680202	Scheible et al. (2011)	M1b2
Kuwait	HQ680203	Scheible et al. (2011)	I1d
Kuwait	HQ680204	Scheible et al. (2011)	X2e2a2
Kuwait	HQ680205	Scheible et al. (2011)	J2a2a1a
Kuwait	HQ680206	Scheible et al. (2011)	L2a1+143+@16309
Kuwait	HQ680207	Scheible et al. (2011)	X2+225
Kuwait	HQ680208	Scheible et al. (2011)	N1a3a
Kuwait	HQ680209	Scheible et al. (2011)	M18'38
Kuwait	HQ680210	Scheible et al. (2011)	N1a1b1
Kuwait	HQ680211	Scheible et al. (2011)	N1a3a
Kuwait	HQ680212	Scheible et al. (2011)	N1a3a
Kuwait	HQ680213	Scheible et al. (2011)	N3
Kuwait	HQ680214	Scheible et al. (2011)	U7
Kuwait	HQ680215	Scheible et al. (2011)	L3h1a2a
Kuwait	HQ680216	Scheible et al. (2011)	N1a3a
Kuwait	HQ680217	Scheible et al. (2011)	B4c2
Kuwait	HQ680218	Scheible et al. (2011)	H82
Kuwait	HQ680219	Scheible et al. (2011)	HV1
Kuwait	HQ680220	Scheible et al. (2011)	J1b1b
Kuwait	HQ680221	Scheible et al. (2011)	W4
Kuwait	HQ680222	Scheible et al. (2011)	M38a
Kuwait	HQ680223	Scheible et al. (2011)	T2c1a
Kuwait	HQ680224	Scheible et al. (2011)	N3
Kuwait	HQ680225	Scheible et al. (2011)	N1a3a
Kuwait	HQ680226	Scheible et al. (2011)	H8a1
Kuwait	HQ680227	Scheible et al. (2011)	H57
Kuwait	HQ680228	Scheible et al. (2011)	J1b2a
Kuwait	HQ680229	Scheible et al. (2011)	M1a1
Kuwait	HQ680230	Scheible et al. (2011)	H7f
Kuwait	HQ680231	Scheible et al. (2011)	R0a1a
Kuwait	HQ680232	Scheible et al. (2011)	L0g

Population	GenBank	Reference	Haplogroup (HG)
Kuwait	HQ680233	Scheible et al. (2011)	U9a
Kuwait	HQ680234	Scheible et al. (2011)	R0a1a
Kuwait	HQ680235	Scheible et al. (2011)	U6a'b'd+16311
Kuwait	HQ680236	Scheible et al. (2011)	L3e1a2
Kuwait	HQ680237	Scheible et al. (2011)	M30+16234
Kuwait	HQ680238	Scheible et al. (2011)	H3s
Kuwait	HQ680239	Scheible et al. (2011)	H57
Kuwait	HQ680240	Scheible et al. (2011)	M30+16234
Kuwait	HQ680241	Scheible et al. (2011)	T2b7a2
Kuwait	HQ680242	Scheible et al. (2011)	H2a2a
Kuwait	HQ680243	Scheible et al. (2011)	HV14
Kuwait	HQ680244	Scheible et al. (2011)	K1a
Kuwait	HQ680245	Scheible et al. (2011)	J1d1a
Kuwait	HQ680246	Scheible et al. (2011)	J2a2a1a
Kuwait	HQ680247	Scheible et al. (2011)	K1a+150
Kuwait	HQ680248	Scheible et al. (2011)	K1a4c
Kuwait	HQ680249	Scheible et al. (2011)	T1a2b
Kuwait	HQ680250	Scheible et al. (2011)	X4
Kuwait	HQ680251	Scheible et al. (2011)	M1
Kuwait	HQ680252	Scheible et al. (2011)	N1a1a
Kuwait	HQ680253	Scheible et al. (2011)	R0a2i
Kuwait	HQ680254	Scheible et al. (2011)	X2b+226
Kuwait	HQ680255	Scheible et al. (2011)	N1b1
Kuwait	HQ680256	Scheible et al. (2011)	M65a+@16311
Kuwait	HQ680257	Scheible et al. (2011)	L2c2b
Kuwait	HQ680258	Scheible et al. (2011)	U7a2a
Kuwait	HQ680259	Scheible et al. (2011)	U4
Kuwait	HQ680260	Scheible et al. (2011)	M65a+@16311
Kuwait	HQ680261	Scheible et al. (2011)	J1c
Kuwait	HQ680262	Scheible et al. (2011)	T3
Kuwait	HQ680263	Scheible et al. (2011)	L3e1a1
Kuwait	HQ680264	Scheible et al. (2011)	J1b
Kuwait	HQ680265	Scheible et al. (2011)	T1b
Kuwait	HQ680266	Scheible et al. (2011)	L2c2b
Kuwait	HQ680267	Scheible et al. (2011)	N3
Kuwait	HQ680268	Scheible et al. (2011)	H1+16189

Population	GenBank	Reference	Haplogroup (HG)
Kuwait	HQ680269	Scheible et al. (2011)	L2a1b1a
Kuwait	HQ680270	Scheible et al. (2011)	L1c3a
Kuwait	HQ680271	Scheible et al. (2011)	L3f1b+16292
Kuwait	HQ680272	Scheible et al. (2011)	HV2
Kuwait	HQ680273	Scheible et al. (2011)	U8b1b
Kuwait	HQ680274	Scheible et al. (2011)	T
Kuwait	HQ680275	Scheible et al. (2011)	T
Kuwait	HQ680276	Scheible et al. (2011)	H1bv1
Kuwait	HQ680277	Scheible et al. (2011)	L2a1a2
Kuwait	HQ680278	Scheible et al. (2011)	J1b
Kuwait	HQ680279	Scheible et al. (2011)	L4a1
Kuwait	HQ680280	Scheible et al. (2011)	HV1a1
Kuwait	HQ680281	Scheible et al. (2011)	J1b1b
Kuwait	HQ680282	Scheible et al. (2011)	U7a
Kuwait	HQ680283	Scheible et al. (2011)	W+194
Kuwait	HQ680284	Scheible et al. (2011)	B5
Kuwait	HQ680285	Scheible et al. (2011)	HV4a
Kuwait	HQ680286	Scheible et al. (2011)	L3d1a1a
Kuwait	HQ680287	Scheible et al. (2011)	R2
Kuwait	HQ680288	Scheible et al. (2011)	U7a4a1
Kuwait	HQ680289	Scheible et al. (2011)	H2a5b2
Kuwait	HQ680290	Scheible et al. (2011)	H42a
Kuwait	HQ680291	Scheible et al. (2011)	H2a2a
Kuwait	HQ680292	Scheible et al. (2011)	H1ap1
Kuwait	HQ680293	Scheible et al. (2011)	J1b1b
Kuwait	HQ680294	Scheible et al. (2011)	T1a2b
Kuwait	HQ680295	Scheible et al. (2011)	M7c
Kuwait	HQ680296	Scheible et al. (2011)	N1a3a
Kuwait	HQ680297	Scheible et al. (2011)	HV1
Kuwait	HQ680298	Scheible et al. (2011)	R0a2c
Kuwait	HQ680299	Scheible et al. (2011)	R0a1a
Kuwait	HQ680300	Scheible et al. (2011)	T2b23
Kuwait	HQ680301	Scheible et al. (2011)	U6a7b1
Kuwait	HQ680302	Scheible et al. (2011)	J1b8
Kuwait	HQ680303	Scheible et al. (2011)	M6
Kuwait	HQ680304	Scheible et al. (2011)	T2g1b

Population	GenBank	Reference	Haplogroup (HG)
Kuwait	HQ680305	Scheible et al. (2011)	H1cf
Kuwait	HQ680306	Scheible et al. (2011)	J1b1a1a
Kuwait	HQ680307	Scheible et al. (2011)	L0a2a2
Kuwait	HQ680308	Scheible et al. (2011)	T2b+16362
Kuwait	HQ680309	Scheible et al. (2011)	U5a1+@16192
Kuwait	HQ680310	Scheible et al. (2011)	H57
Kuwait	HQ680311	Scheible et al. (2011)	R0a2c
Kuwait	HQ680312	Scheible et al. (2011)	I1
Kuwait	HQ680313	Scheible et al. (2011)	T
Kuwait	HQ680314	Scheible et al. (2011)	T1b
Kuwait	HQ680315	Scheible et al. (2011)	H3b6
Kuwait	HQ680316	Scheible et al. (2011)	U7a4a1
Kuwait	HQ680317	Scheible et al. (2011)	U2e1'2'3
Kuwait	HQ680318	Scheible et al. (2011)	R0a
Kuwait	HQ680319	Scheible et al. (2011)	J1b
Kuwait	HQ680320	Scheible et al. (2011)	J1b8
Kuwait	HQ680321	Scheible et al. (2011)	I7
Kuwait	HQ680322	Scheible et al. (2011)	H57
Kuwait	HQ680323	Scheible et al. (2011)	H57
Kuwait	HQ680324	Scheible et al. (2011)	L1c1
Kuwait	HQ680325	Scheible et al. (2011)	H101
Kuwait	HQ680326	Scheible et al. (2011)	U6a'b'd+16311
Kuwait	HQ680327	Scheible et al. (2011)	R0a1a
Kuwait	HQ680328	Scheible et al. (2011)	J2a2a1a
Kuwait	HQ680329	Scheible et al. (2011)	J1b
Kuwait	HQ680330	Scheible et al. (2011)	H57
Kuwait	HQ680331	Scheible et al. (2011)	U2b2
Kuwait	HQ680332	Scheible et al. (2011)	N1b1
Kuwait	HQ680333	Scheible et al. (2011)	K1a8a
Kuwait	HQ680334	Scheible et al. (2011)	L2a1c+16129
Kuwait	HQ680335	Scheible et al. (2011)	U3b3
Kuwait	HQ680336	Scheible et al. (2011)	H14a
Kuwait	HQ680337	Scheible et al. (2011)	R0a1b
Kuwait	HQ680338	Scheible et al. (2011)	HV13a
Kazakhstan	GU069433	Irwin et al. (2010)	U2e1'2'3
Kazakhstan	GU069434	Irwin et al. (2010)	H2a2a

Population	GenBank	Reference	Haplogroup (HG)
Kazakhstan	GU069435	Irwin et al. (2010)	K1a
Kazakhstan	GU069436	Irwin et al. (2010)	U2e1
Kazakhstan	GU069437	Irwin et al. (2010)	N1b1
Kazakhstan	GU069438	Irwin et al. (2010)	Z+152
Kazakhstan	GU069439	Irwin et al. (2010)	T2b
Kazakhstan	GU069440	Irwin et al. (2010)	A23
Kazakhstan	GU069441	Irwin et al. (2010)	U5a1+@16192
Kazakhstan	GU069442	Irwin et al. (2010)	K1c1e
Kazakhstan	GU069443	Irwin et al. (2010)	G2a2a
Kazakhstan	GU069444	Irwin et al. (2010)	X2i
Kazakhstan	GU069445	Irwin et al. (2010)	K1a
Kazakhstan	GU069446	Irwin et al. (2010)	G2a+152
Kazakhstan	GU069447	Irwin et al. (2010)	U5a2
Kazakhstan	GU069448	Irwin et al. (2010)	H2a+152 16311
Kazakhstan	GU069449	Irwin et al. (2010)	N9a
Kazakhstan	GU069450	Irwin et al. (2010)	G2a+152
Kazakhstan	GU069451	Irwin et al. (2010)	H1b1+16362
Kazakhstan	GU069452	Irwin et al. (2010)	C4a1a+195
Kazakhstan	GU069453	Irwin et al. (2010)	D4c2a
Kazakhstan	GU069454	Irwin et al. (2010)	H5
Kazakhstan	GU069455	Irwin et al. (2010)	C
Kazakhstan	GU069456	Irwin et al. (2010)	U4b1a3
Kazakhstan	GU069457	Irwin et al. (2010)	M7b1b
Kazakhstan	GU069458	Irwin et al. (2010)	M43a1
Kazakhstan	GU069459	Irwin et al. (2010)	A8a1
Kazakhstan	GU069460	Irwin et al. (2010)	C5a
Kazakhstan	GU069461	Irwin et al. (2010)	C4a1a3d
Kazakhstan	GU069462	Irwin et al. (2010)	H6
Kazakhstan	GU069463	Irwin et al. (2010)	C4a2a1
Kazakhstan	GU069464	Irwin et al. (2010)	U5b2a1b
Kazakhstan	GU069465	Irwin et al. (2010)	M10a2
Kazakhstan	GU069466	Irwin et al. (2010)	H14b1
Kazakhstan	GU069467	Irwin et al. (2010)	F1a1
Kazakhstan	GU069468	Irwin et al. (2010)	T2c1f
Kazakhstan	GU069469	Irwin et al. (2010)	U5a1+@16192
Kazakhstan	GU069470	Irwin et al. (2010)	C4a1a3d

Population	GenBank	Reference	Haplogroup (HG)
Kazakhstan	GU069471	Irwin et al. (2010)	T1a1m
Kazakhstan	GU069472	Irwin et al. (2010)	J1b
Kazakhstan	GU069473	Irwin et al. (2010)	A8a1
Kazakhstan	GU069474	Irwin et al. (2010)	T2g1
Kazakhstan	GU069475	Irwin et al. (2010)	H1b1+16362
Kazakhstan	GU069476	Irwin et al. (2010)	F1b1b
Kazakhstan	GU069477	Irwin et al. (2010)	U1a3
Kazakhstan	GU069478	Irwin et al. (2010)	A+152+16362
Kazakhstan	GU069479	Irwin et al. (2010)	U5a2a
Kazakhstan	GU069480	Irwin et al. (2010)	M9
Kazakhstan	GU069481	Irwin et al. (2010)	HV14
Kazakhstan	GU069482	Irwin et al. (2010)	D4c1b
Kazakhstan	GU069483	Irwin et al. (2010)	G2a+152
Kazakhstan	GU069484	Irwin et al. (2010)	H6b2
Kazakhstan	GU069485	Irwin et al. (2010)	G2a2a
Kazakhstan	GU069486	Irwin et al. (2010)	U5a1h
Kazakhstan	GU069487	Irwin et al. (2010)	M9
Kazakhstan	GU069488	Irwin et al. (2010)	U4b3
Kazakhstan	GU069489	Irwin et al. (2010)	D4h2
Kazakhstan	GU069490	Irwin et al. (2010)	D4j2
Kazakhstan	GU069491	Irwin et al. (2010)	A11
Kazakhstan	GU069492	Irwin et al. (2010)	M3d
Kazakhstan	GU069493	Irwin et al. (2010)	U2c'd
Kazakhstan	GU069494	Irwin et al. (2010)	G2a+152
Kazakhstan	GU069495	Irwin et al. (2010)	M9a1a1a
Kazakhstan	GU069496	Irwin et al. (2010)	G2a+152
Kazakhstan	GU069497	Irwin et al. (2010)	T
Kazakhstan	GU069498	Irwin et al. (2010)	H2a2a
Kazakhstan	GU069499	Irwin et al. (2010)	H1j8
Kazakhstan	GU069500	Irwin et al. (2010)	D4o1
Kazakhstan	GU069501	Irwin et al. (2010)	D4e5a
Kazakhstan	GU069502	Irwin et al. (2010)	D4c2a
Kazakhstan	GU069503	Irwin et al. (2010)	M8a2a1
Kazakhstan	GU069504	Irwin et al. (2010)	D4a3
Kazakhstan	GU069504	Irwin et al. (2010)	U8b1b
Kazakhstan	GU069506	Irwin et al. (2010)	N9a1'3

Population	GenBank	Reference	Haplogroup (HG)
Kazakhstan	GU069507	Irwin et al. (2010)	G2a5
Kazakhstan	GU069508	Irwin et al. (2010)	D4e1a2a
Kazakhstan	GU069509	Irwin et al. (2010)	G2a5
Kazakhstan	GU069510	Irwin et al. (2010)	HV2a
Kazakhstan	GU069511	Irwin et al. (2010)	H1e1b
Kazakhstan	GU069512	Irwin et al. (2010)	A14
Kazakhstan	GU069513	Irwin et al. (2010)	U4a2
Kazakhstan	GU069514	Irwin et al. (2010)	H1+16189
Kazakhstan	GU069515	Irwin et al. (2010)	H2a1
Kazakhstan	GU069516	Irwin et al. (2010)	T2b34
Kazakhstan	GU069517	Irwin et al. (2010)	J1b1a1
Kazakhstan	GU069518	Irwin et al. (2010)	R2
Kazakhstan	GU069519	Irwin et al. (2010)	D4o2a
Kazakhstan	GU069520	Irwin et al. (2010)	HV2a
Kazakhstan	GU069521	Irwin et al. (2010)	C5a
Kazakhstan	GU069522	Irwin et al. (2010)	U4
Kazakhstan	GU069523	Irwin et al. (2010)	K2a5
Kazakhstan	GU069524	Irwin et al. (2010)	HV0
Kazakhstan	GU069525	Irwin et al. (2010)	D4j+(16286)
Kazakhstan	GU069526	Irwin et al. (2010)	M7b1a1+(16192)
Kazakhstan	GU069527	Irwin et al. (2010)	U5b2a2
Kazakhstan	GU069528	Irwin et al. (2010)	D4o2a
Kazakhstan	GU069529	Irwin et al. (2010)	U4
Kazakhstan	GU069530	Irwin et al. (2010)	D4c2a
Kazakhstan	GU069531	Irwin et al. (2010)	H15
Kazakhstan	GU069532	Irwin et al. (2010)	G2a5
Kazakhstan	GU069533	Irwin et al. (2010)	J1b1a1
Kazakhstan	GU069534	Irwin et al. (2010)	C4a2a1
Kazakhstan	GU069535	Irwin et al. (2010)	A
Kazakhstan	GU069536	Irwin et al. (2010)	J1b1a1
Kazakhstan	GU069537	Irwin et al. (2010)	N9a1'3
Kazakhstan	GU069538	Irwin et al. (2010)	D4o2a
Kazakhstan	GU069539	Irwin et al. (2010)	U1a1a1
Kazakhstan	GU069540	Irwin et al. (2010)	U7a
Kazakhstan	GU069541	Irwin et al. (2010)	A24
Kazakhstan	GU069542	Irwin et al. (2010)	F1b1+@152

Population	GenBank	Reference	Haplogroup (HG)
Kazakhstan	GU069543	Irwin et al. (2010)	U5b1b1+@16192
Kazakhstan	GU069544	Irwin et al. (2010)	F1a1
Kazakhstan	GU069545	Irwin et al. (2010)	A24
Kazakhstan	GU069546	Irwin et al. (2010)	A+152+16362
Kazakhstan	GU069547	Irwin et al. (2010)	G1a3
Kazakhstan	GU069548	Irwin et al. (2010)	C5a
Kazakhstan	GU069549	Irwin et al. (2010)	U5a1+@16192
Kazakhstan	GU069550	Irwin et al. (2010)	C4a1a4a
Kazakhstan	GU069551	Irwin et al. (2010)	D4c1b
Kazakhstan	GU069552	Irwin et al. (2010)	D4h1
Kazakhstan	GU069553	Irwin et al. (2010)	T2b34
Kazakhstan	GU069554	Irwin et al. (2010)	F1b1+@152
Kazakhstan	GU069555	Irwin et al. (2010)	M9
Kazakhstan	GU069556	Irwin et al. (2010)	A+152+16362
Kazakhstan	GU069557	Irwin et al. (2010)	H2a2a
Kazakhstan	GU069558	Irwin et al. (2010)	H6b2
Kazakhstan	GU069559	Irwin et al. (2010)	U5b2b1a
Kazakhstan	GU069560	Irwin et al. (2010)	T2f7a
Kazakhstan	GU069561	Irwin et al. (2010)	C4a1a+195
Kazakhstan	GU069562	Irwin et al. (2010)	T2b
Kazakhstan	GU069563	Irwin et al. (2010)	HV0
Kazakhstan	GU069564	Irwin et al. (2010)	U2e1h
Kazakhstan	GU069565	Irwin et al. (2010)	H2a2a
Kazakhstan	GU069566	Irwin et al. (2010)	A8a1
Kazakhstan	GU069567	Irwin et al. (2010)	D5b
Kazakhstan	GU069568	Irwin et al. (2010)	H6
Kazakhstan	GU069569	Irwin et al. (2010)	U2e1'2'3
Kazakhstan	GU069570	Irwin et al. (2010)	H1c
Kazakhstan	GU069571	Irwin et al. (2010)	M8a2'3
Kazakhstan	GU069572	Irwin et al. (2010)	D4b1a2a1
Kazakhstan	GU069573	Irwin et al. (2010)	H2a1
Kazakhstan	GU069574	Irwin et al. (2010)	A
Kazakhstan	GU069575	Irwin et al. (2010)	H5a5
Kazakhstan	GU069576	Irwin et al. (2010)	F1a1
Kazakhstan	GU069577	Irwin et al. (2010)	A5a
Kazakhstan	GU069578	Irwin et al. (2010)	A24

Population	GenBank	Reference	Haplogroup (HG)
Kazakhstan	GU069579	Irwin et al. (2010)	H10+(16093)
Kazakhstan	GU069580	Irwin et al. (2010)	M36
Kazakhstan	GU069581	Irwin et al. (2010)	D4i
Kazakhstan	GU069582	Irwin et al. (2010)	U5a2b1b
Kazakhstan	GU069583	Irwin et al. (2010)	C
Kazakhstan	GU069584	Irwin et al. (2010)	U5a2a
Kazakhstan	GU069585	Irwin et al. (2010)	F1b1+@152
Kazakhstan	GU069586	Irwin et al. (2010)	D4b1a1
Kazakhstan	GU069587	Irwin et al. (2010)	A19
Kazakhstan	GU069588	Irwin et al. (2010)	U2e1
Kazakhstan	GU069589	Irwin et al. (2010)	F1b1b
Kazakhstan	GU069590	Irwin et al. (2010)	U7a
Kazakhstan	GU069591	Irwin et al. (2010)	G2b1b
Kazakhstan	GU069592	Irwin et al. (2010)	D4b1a2a1
Kazakhstan	GU069593	Irwin et al. (2010)	D4c2b
Kazakhstan	GU069594	Irwin et al. (2010)	B4a2b
Kazakhstan	GU069595	Irwin et al. (2010)	C4e
Kazakhstan	GU069596	Irwin et al. (2010)	Z1a
Kazakhstan	GU069597	Irwin et al. (2010)	T2a1b
Kazakhstan	GU069598	Irwin et al. (2010)	M9
Kazakhstan	GU069599	Irwin et al. (2010)	T2
Kazakhstan	GU069600	Irwin et al. (2010)	M37+152+151
Kazakhstan	GU069601	Irwin et al. (2010)	G2a2a
Kazakhstan	GU069602	Irwin et al. (2010)	C4a1a+195
Kazakhstan	GU069603	Irwin et al. (2010)	B4b1a3a
Kazakhstan	GU069604	Irwin et al. (2010)	HV2a
Kazakhstan	GU069605	Irwin et al. (2010)	D4h2
Kazakhstan	GU069606	Irwin et al. (2010)	M9a1a1a
Kazakhstan	GU069607	Irwin et al. (2010)	J2b1a
Kazakhstan	GU069608	Irwin et al. (2010)	C5b1b
Kazakhstan	GU069609	Irwin et al. (2010)	D4b1c
Kazakhstan	GU069610	Irwin et al. (2010)	C
Kazakhstan	GU069611	Irwin et al. (2010)	I4a1
Kazakhstan	GU069612	Irwin et al. (2010)	U5b2a1b
Kazakhstan	GU069613	Irwin et al. (2010)	A+152+16362
Kazakhstan	GU069614	Irwin et al. (2010)	W+194

Population	GenBank	Reference	Haplogroup (HG)
Kazakhstan	GU069615	Irwin et al. (2010)	G1a1
Kazakhstan	GU069616	Irwin et al. (2010)	M10a2
Kazakhstan	GU069617	Irwin et al. (2010)	D4b1a2a1
Kazakhstan	GU069618	Irwin et al. (2010)	K1a
Kazakhstan	GU069619	Irwin et al. (2010)	D4m2a
Kazakhstan	GU069620	Irwin et al. (2010)	D4h1
Kazakhstan	GU069621	Irwin et al. (2010)	H1c
Kazakhstan	GU069622	Irwin et al. (2010)	U2e1
Kazakhstan	GU069623	Irwin et al. (2010)	N9a5
Kazakhstan	GU069624	Irwin et al. (2010)	A16
Kazakhstan	GU069625	Irwin et al. (2010)	M9
Kazakhstan	GU069626	Irwin et al. (2010)	Z+152
Kazakhstan	GU069627	Irwin et al. (2010)	B4a1c3
Kazakhstan	GU069628	Irwin et al. (2010)	B4
Kazakhstan	GU069629	Irwin et al. (2010)	C5a
Kazakhstan	GU069630	Irwin et al. (2010)	F2a
Kazakhstan	GU069631	Irwin et al. (2010)	M13'46'61+16362
Kazakhstan	GU069632	Irwin et al. (2010)	G2a+152
Kazakhstan	GU069633	Irwin et al. (2010)	I
Kazakhstan	GU069634	Irwin et al. (2010)	D4b1a1
Kazakhstan	GU069635	Irwin et al. (2010)	D4o2a
Kazakhstan	GU069636	Irwin et al. (2010)	M9a'b
Kazakhstan	GU069637	Irwin et al. (2010)	U2e1b1
Kazakhstan	GU069638	Irwin et al. (2010)	D4i
Kazakhstan	GU069639	Irwin et al. (2010)	R0a+60. 1T
Kazakhstan	GU069640	Irwin et al. (2010)	C4a1a+195
Kazakhstan	GU069641	Irwin et al. (2010)	D4i
Kazakhstan	GU069642	Irwin et al. (2010)	D4h1
Kazakhstan	GU069643	Irwin et al. (2010)	H6a1b3
Kazakhstan	GU069644	Irwin et al. (2010)	D4n
Kazakhstan	GU069645	Irwin et al. (2010)	J1
Kazakhstan	GU069646	Irwin et al. (2010)	H15
Kazakhstan	GU069647	Irwin et al. (2010)	D5b
Kazakhstan	GU069648	Irwin et al. (2010)	C4a2a
Kazakhstan	GU069649	Irwin et al. (2010)	B5b4
Kazakhstan	GU069650	Irwin et al. (2010)	H3h2

Population	GenBank	Reference	Haplogroup (HG)
Kazakhstan	GU069651	Irwin et al. (2010)	G2a
Kazakhstan	GU069652	Irwin et al. (2010)	G2a+152
Kazakhstan	GU069653	Irwin et al. (2010)	H14a
Kazakhstan	GU069654	Irwin et al. (2010)	HV0
Kazakhstan	GU069655	Irwin et al. (2010)	T1a1'3
Kazakhstan	GU069656	Irwin et al. (2010)	A8a1
Kazakhstan	GU069657	Irwin et al. (2010)	D5a2a1
Kazakhstan	GU069658	Irwin et al. (2010)	H1c
Kazakhstan	GU069659	Irwin et al. (2010)	D4q
Kazakhstan	GU069660	Irwin et al. (2010)	H2a2a
Kazakhstan	GU069661	Irwin et al. (2010)	U2b2
Kazakhstan	GU069662	Irwin et al. (2010)	HV1
Kazakhstan	GU069663	Irwin et al. (2010)	A15
Kazakhstan	GU069664	Irwin et al. (2010)	J1d
Kazakhstan	GU069665	Irwin et al. (2010)	N1a1a1a1a
Kazakhstan	GU069666	Irwin et al. (2010)	U5b1e
Kazakhstan	GU069667	Irwin et al. (2010)	G2b1b
Kazakhstan	GU069668	Irwin et al. (2010)	J1b1a1
Kazakhstan	GU069669	Irwin et al. (2010)	W4
Kazakhstan	GU069670	Irwin et al. (2010)	H1b
Kazakhstan	GU069671	Irwin et al. (2010)	H1e+16129
Kazakhstan	GU069672	Irwin et al. (2010)	B4c1b
Kazakhstan	GU069673	Irwin et al. (2010)	U4a2
Kazakhstan	GU069674	Irwin et al. (2010)	D4m2
Kazakhstan	GU069675	Irwin et al. (2010)	HV4b
Kazakhstan	GU069676	Irwin et al. (2010)	F
Kazakhstan	GU069677	Irwin et al. (2010)	H5+16192
Kazakhstan	GU069678	Irwin et al. (2010)	W4
Kazakhstan	GU069679	Irwin et al. (2010)	H2a1f
Kazakhstan	GU069680	Irwin et al. (2010)	T1a1'3
Kazakhstan	GU069681	Irwin et al. (2010)	H2a2a
Kazakhstan	GU069682	Irwin et al. (2010)	C5
Kazakhstan	GU069683	Irwin et al. (2010)	K1a4a1c1
Kazakhstan	GU069684	Irwin et al. (2010)	A+152+16362
Kazakhstan	GU069685	Irwin et al. (2010)	D4j1b2
Kazakhstan	GU069686	Irwin et al. (2010)	H1aj1

Population	GenBank	Reference	Haplogroup (HG)
Kazakhstan	GU069687	Irwin et al. (2010)	HV6
Kazakhstan	GU069688	Irwin et al. (2010)	F1a1
Lebanon	JQ797965	Pala et al. (2012)	J2b1e
Lebanon	DQ301816	Behar et al. (2006)	K1a8
Lebanon	KC867118	Kushniarevich et al. (2013)	N1a3a
Lebanon	KP407062	Gandini et al. (unpub)	R0a2n
Lebanon	KP407066	Gandini et al. (unpub)	R0a2r
Lebanon	KT779157	Zalloua et al. (unpub)	U1b3
Lebanon	KT779158	Zalloua et al. (unpub)	U1b3
Lebanon	KT779159	Zalloua et al. (unpub)	U3b1
Lebanon	KT779160	Zalloua et al. (unpub)	U3b2
Lebanon	KT779161	Zalloua et al. (unpub)	U3b2
Lebanon	KT779162	Zalloua et al. (unpub)	U3b2
Lebanon	KT779163	Zalloua et al. (unpub)	U3a
Lebanon	KT779164	Zalloua et al. (unpub)	U8a1a
Lebanon	KT779165	Zalloua et al. (unpub)	U3b2a
Lebanon	KT779166	Zalloua et al. (unpub)	U5a1g
Lebanon	KT779167	Zalloua et al. (unpub)	U1a1a
Lebanon	KT779168	Zalloua et al. (unpub)	U3b2
Lebanon	KT779169	Zalloua et al. (unpub)	U3b2a
Lebanon	KT779170	Zalloua et al. (unpub)	U3b2a
Lebanon	KT779171	Zalloua et al. (unpub)	U6a7a1b
Lithuania	JQ797800	Pala et al. (2012)	J1c2a
Lithuania	JQ797908	Pala et al. (2012)	J2a1a2
Lithuania	KU052787	direct submission	I1c1a
Lithuania	KJ816752	direct submission	I1a1a
Lithuania	KJ558222	direct submission	I1
Lithuania	KF577586	direct submission	T2e1b1
Lithuania	EU148452	direct submission	H1e4a
Lithuania	JN086657	direct submission	T2g1
Lithuania	EF421157	direct submission	HV1
Lithuania	EF396958	direct submission	HV1
Lithuania	HM627319	direct submission	J1c7a
Lithuania	HM627319	Pala et al. (2012) misc.	J1c7a
Mansi	EU007880	Ingman and Gyllensten (2007)	J1d6a
Mansi	EU007879	Ingman and Gyllensten (2007)	C4b1

Population	GenBank	Reference	Haplogroup (HG)
Mansi	EU007878	Ingman and Gyllensten (2007)	H27a
Mansi	EU007877	Ingman and Gyllensten (2007)	D4j2a
Mansi	AY570524	Starikovskaya et al. (2005)	D5a3a1a
Mansi	AY519488.1	Starikovskaya et al. (2005)	A12a
Mansi	JN375993	Sukernik et al. (2012)	D4*
Mansi	FJ858884	Sukernik et al. (2012)	D3a1
Mansi	FJ858878	Sukernik et al. (2012)	U7
Mansi	FJ858877	Sukernik et al. (2012)	U4b
Mansi	FJ493507	Sukernik et al. (2012)	U4a
Mansi	FJ147322	Sukernik et al. (2012)	U4c
Moldova	JQ797944	Pala et al. (2012)	J2b1a
Moldova	KP340173	DeFanti et al. (2015)	HV4c
Moldova	HQ699439	direct submission	H
Moldova	HQ663853	direct submission	H5
Mongolia	JN857056	Derenko et al. (2012)	M9a1b1*
Mongolia	JN857055	Derenko et al. (2012)	M10a1a1
Mongolia	EU007893	Ingman and Gyllensten (2007)	D5c+16311
Mongolia	EU007892	Ingman and Gyllensten (2007)	Y1a
Mongolia	EU007891	Ingman and Gyllensten (2007)	U4d2
Mongolia	EU007890	Ingman and Gyllensten (2007)	M7c1a1a1
Mongolia	DQ437577	Pala et al. (2012) misc.	T2d1
Mongolia	AY255146	Kong et al. (2003)	M7c1c2
Mongolia	KF146280	Olivieri et al. (2013)	W4a
Negidal	AY519489.2	Starikovskaya et al. (2005)	B5b2a
Negidal	AY195792.2	Mishmar et al. (2003)	Y1a+16189
Negidal	AY195790.2	Mishmar et al. (2003)	D4o2a
Negidal	EU482365	Volodko et al. (2008)	D4a
Negidal	EU482366	Volodko et al. (2008)	D4
Negidal	EU482367	Volodko et al. (2008)	D4I2a2
Nepal	JQ798064	Pala et al. (2012)	T2b4
Nepal	JQ798065	Pala et al. (2012)	T2b4
Nepal	FJ770971.1	Fornarino et al. (2009)	M4c
Nepal	FJ770968	Fornarino et al. (2009)	M33b
Nepal	FJ770967	Fornarino et al. (2009)	F1d
Nepal	FJ770966	Fornarino et al. (2009)	M35b
Nepal	FJ770965	Fornarino et al. (2009)	M51

Population	GenBank	Reference	Haplogroup (HG)
Nepal	FJ770964	Fornarino et al. (2009)	M52
Nepal	FJ770963	Fornarino et al. (2009)	M38
Nepal	FJ770962	Fornarino et al. (2009)	M31b1
Nepal	FJ770961	Fornarino et al. (2009)	R30a
Nepal	FJ770960	Fornarino et al. (2009)	M33a
Nepal	FJ770959	Fornarino et al. (2009)	M33a
Nepal	FJ770958	Fornarino et al. (2009)	M43a
Nepal	FJ770957	Fornarino et al. (2009)	M21b
Nepal	FJ770956	Fornarino et al. (2009)	M35
Nepal	FJ770955	Fornarino et al. (2009)	M5a
Nepal	FJ770954	Fornarino et al. (2009)	M
Nepal	FJ770953	Fornarino et al. (2009)	M
Nepal	JF742209.2	Wang et al. (unpub)	M35b+16304
Nganasan	AY615359	Starikovskaya et al. (2005)	C5b1a
Nganasan	AY519490.2	Starikovskaya et al. (2005)	C4b8a
Nganasan	AY519491.2	Starikovskaya et al. (2005)	D4o2a
Nganasan	FJ493513	Sukernik et al. (2012)	Z1a
Nganasan	FJ493506	Sukernik et al. (2012)	U4a
Nganasan	EU482368	Volodko et al. (2008)	C2a
Nganasan	EU482369	Volodko et al. (2008)	D6
Nganasan	EU482370	Volodko et al. (2008)	C2a
Nganasan	EU482371	Volodko et al. (2008)	C2b
Nganasan	EU482372	Volodko et al. (2008)	D3
Nganasan	FJ230891	Volodko et al. (2008)	U4c
Nganasan	EU660537	Derbeneva et al. (2002)	D3
Nivkhi	KF148336	Duggan et al. (2013)	D4m2a
Nivkhi	KF148337	Duggan et al. (2013)	Y1a+16189
Nivkhi	KF148338	Duggan et al. (2013)	G1b1
Nivkhi	KF148339	Duggan et al. (2013)	Y1a+16189
Nivkhi	KF148340	Duggan et al. (2013)	Y1a+16189
Nivkhi	KF148341	Duggan et al. (2013)	Y1a+16189
Nivkhi	KF148342	Duggan et al. (2013)	Y1a+16189
Nivkhi	KF148343	Duggan et al. (2013)	Y1a+16189
Nivkhi	KF148344	Duggan et al. (2013)	Y1a+16189
Nivkhi	KF148345	Duggan et al. (2013)	Y1a+16189
Nivkhi	KF148346	Duggan et al. (2013)	Y1a+16189

Population	GenBank	Reference	Haplogroup (HG)
Nivkhi	KF148347	Duggan et al. (2013)	Y1a+16189
Nivkhi	KF148348	Duggan et al. (2013)	Y1a+16189
Nivkhi	KF148349	Duggan et al. (2013)	Y1a+16189
Nivkhi	KF148350	Duggan et al. (2013)	D4m2a
Nivkhi	KF148351	Duggan et al. (2013)	D4m2a
Nivkhi	KF148352	Duggan et al. (2013)	Y1a+16189
Nivkhi	KF148353	Duggan et al. (2013)	Y1a+16189
Nivkhi	KF148354	Duggan et al. (2013)	Y1a+16189
Nivkhi	KF148355	Duggan et al. (2013)	D4m2a
North Ossetian	JQ797898	Pala et al. (2012)	J1d2c
North Ossetian	JQ797966	Pala et al. (2012)	J2b1
North Ossetian	JQ797989	Pala et al. (2012)	T1a1a1
North Ossetian	AM263177	Roostalu et al. (2007)	H6a1a1
North Ossetian	JQ245723	Fernandes et al. (2012)	W6
North Ossetian	JQ797777	Pala et al. (2012)	J1b5a
North Ossetian	JQ797894	Pala et al. (2012)	J1d2b
North Ossetian	KC152591	Pennarun et al. (2012)	M1a1b1b
North Ossetian	JQ245724	Fernandes et al. (2012)	I5
North Ossetian	JQ245726	Fernandes et al. (2012)	X2f
North Ossetian	JQ245727	Fernandes et al. (2012)	N1b1
North Ossetian	JQ245736	Fernandes et al. (2012)	W6
North Ossetian	JQ245737	Fernandes et al. (2012)	I4
North Ossetian	JQ245738	Fernandes et al. (2012)	X2f
Pakistan	AY882391.2	Achilli et al. (2005)	U7
Pakistan	AY882390	Achilli et al. (2005)	U9b
Pakistan	AY882381	Achilli et al. (2005)	U2c
Pakistan	AY882380	Achilli et al. (2005)	U2b
Pakistan	AY882379	Achilli et al. (2005)	U2a
Palestine	JQ797909	Pala et al. (2012)	J2a1a2
Palestine	DQ301810	Behar et al. (2006)	K1b1c
Palestine	KP407080	Gandini et al. (unpub)	R0a6
Palestine	KP407026	Gandini et al. (unpub)	R0a1a
Palestine	KP407028	Gandini et al. (unpub)	R0a1a5
Palestine	KP407047	Gandini et al. (unpub)	R0a2b
Palestine	KP407051	Gandini et al. (unpub)	R0a2b2
Palestine	HQ651712	Pereira et al. (2010)	U6a2

Population	GenBank	Reference	Haplogroup (HG)
Palestine	HQ651711	Pereira et al. (2010)	U6a3
Poland	JQ797803	Pala et al. (2012)	J1c2a
Poland	JX266263.1	Mielnik-Sikorska et al. (2013)	L1b1a12b
Poland	JX266264.1	Mielnik-Sikorska et al. (2013)	L2a1I2a
Poland	JX266265.2	Mielnik-Sikorska et al. (2013)	L2a1I2a1
Poland	JX266266.2	Mielnik-Sikorska et al. (2013)	G2a2a
Poland	JX266267.2	Mielnik-Sikorska et al. (2013)	A8a1
Poland	JX266268.1	Mielnik-Sikorska et al. (2013)	C4a1a1
Poland	JX266269.1	Mielnik-Sikorska et al. (2013)	D5a2a1a1
Poland	JX307102	Mielnik-Sikorska et al. (2013)	H6a1b3
Poland	JX307103	Mielnik-Sikorska et al. (2013)	H6a1b3
Poland	JX307110	Mielnik-Sikorska et al. (2013)	H6c1
Poland	JX128041	Mielnik-Sikorska et al. (2013)	H5a2
Poland	JX128042	Mielnik-Sikorska et al. (2013)	H5a1
Poland	JX128043	Mielnik-Sikorska et al. (2013)	H5a1i
Poland	JX128051	Mielnik-Sikorska et al. (2013)	H5a1a
Poland	JX128052	Mielnik-Sikorska et al. (2013)	H5a2
Poland	JX128058	Mielnik-Sikorska et al. (2013)	H5a1
Poland	JX128059	Mielnik-Sikorska et al. (2013)	H5e1a
Poland	JX128062	Mielnik-Sikorska et al. (2013)	H5a1a
Poland	JX128063	Mielnik-Sikorska et al. (2013)	H5a1
Roma	DQ359273	Irwin et al. (2007)	J1b
Roma	DQ359274	Irwin et al. (2007)	J1b
Romania	DQ359275	Irwin et al. (2007)	J1c1b1a
Romania	DQ359276	Irwin et al. (2007)	J1c2a
Romania	DQ359277	Irwin et al. (2007)	J1c2a3a
Romania	DQ359278	Irwin et al. (2007)	J1c2a5
Romania	DQ359279	Irwin et al. (2007)	J1c7
Romania	DQ359280	Irwin et al. (2007)	J1c7
Romania	DQ359281	Irwin et al. (2007)	J1c7
Romania	DQ359282	Irwin et al. (2007)	J2b2
Romania	DQ359283	Irwin et al. (2007)	J1c
Romania	DQ359284	Irwin et al. (2007)	T2
Romania	DQ359285	Irwin et al. (2007)	N1a3a
Romania	DQ359286	Irwin et al. (2007)	N3a
Romania	DQ359287	Irwin et al. (2007)	R0a2r

Population	GenBank	Reference	Haplogroup (HG)
Romania	DQ359288	Irwin et al. (2007)	R0a2r
Romania	DQ359289	Irwin et al. (2007)	R0a2r
Romania	DQ359290	Irwin et al. (2007)	R0a2r
Romania	DQ359291	Irwin et al. (2007)	R0a2r
Roma	DQ359292	Irwin et al. (2007)	I1a1
Roma	DQ359293	Irwin et al. (2007)	M5a1
Roma	DQ359294	Irwin et al. (2007)	M5a1
Roma	DQ359295	Irwin et al. (2007)	J1c1
Roma	DQ359296	Irwin et al. (2007)	M5a1
Roma	DQ359297	Irwin et al. (2007)	M5a1
Roma	DQ359298	Irwin et al. (2007)	N1b1
Roma	DQ359299	Irwin et al. (2007)	N1b1
Roma	DQ359300	Irwin et al. (2007)	J1c2
Roma	DQ359301	Irwin et al. (2007)	HV0
Roma	DQ359302	Irwin et al. (2007)	M5a1
Roma	DQ359303	Irwin et al. (2007)	X2d1
Roma	DQ359304	Irwin et al. (2007)	J1c
Roma	DQ359305	Irwin et al. (2007)	X2b+226
Roma	DQ359306	Irwin et al. (2007)	M5a1
Roma	DQ359307	Irwin et al. (2007)	M5a1
Roma	DQ359308	Irwin et al. (2007)	H1ao
Roma	DQ359309	Irwin et al. (2007)	X2d1
Roma	DQ359310	Irwin et al. (2007)	W+194
Roma	DQ359311	Irwin et al. (2007)	N
Roma	DQ359312	Irwin et al. (2007)	HV0
Roma	DQ359313	Irwin et al. (2007)	N
Roma	DQ359314	Irwin et al. (2007)	M5a1
Roma	DQ359315	Irwin et al. (2007)	M5a1
Roma	DQ359316	Irwin et al. (2007)	M5a1
Roma	DQ359317	Irwin et al. (2007)	M5a1
Roma	DQ359318	Irwin et al. (2007)	X2d1
Roma	DQ359319	Irwin et al. (2007)	X2b+226
Roma	DQ359320	Irwin et al. (2007)	X2b+226
Roma	DQ359321	Irwin et al. (2007)	N
Roma	DQ359322	Irwin et al. (2007)	M5a1
Roma	DQ359323	Irwin et al. (2007)	X2d1

Population	GenBank	Reference	Haplogroup (HG)
Roma	DQ359324	Irwin et al. (2007)	M5a1
Roma	DQ359325	Irwin et al. (2007)	X2d1
Roma	DQ359326	Irwin et al. (2007)	M5a1
Roma	DQ359327	Irwin et al. (2007)	X2d1
Roma	DQ359328	Irwin et al. (2007)	X2b+226
Roma	DQ359329	Irwin et al. (2007)	U2d3
Roma	DQ359330	Irwin et al. (2007)	M5a1
Roma	DQ359331	Irwin et al. (2007)	M35b+16304
Roma	DQ359332	Irwin et al. (2007)	X2d1
Roma	DQ359333	Irwin et al. (2007)	X2d1
Roma	DQ359334	Irwin et al. (2007)	N
Roma	DQ359335	Irwin et al. (2007)	N
Roma	DQ359336	Irwin et al. (2007)	I1a1
Roma	DQ359337	Irwin et al. (2007)	H41a
Roma	DQ359338	Irwin et al. (2007)	M5a1
Roma	DQ359339	Irwin et al. (2007)	X2b+226
Roma	DQ359340	Irwin et al. (2007)	M5a1
Roma	DQ359341	Irwin et al. (2007)	M5a1
Roma	DQ359342	Irwin et al. (2007)	M5a1
Roma	DQ359343	Irwin et al. (2007)	T1a1'3
Roma	DQ359344	Irwin et al. (2007)	T
Roma	DQ359345	Irwin et al. (2007)	M5a1
Roma	DQ359346	Irwin et al. (2007)	X2d1
Roma	DQ359347	Irwin et al. (2007)	M35b+16304
Roma	DQ359348	Irwin et al. (2007)	H1ao
Roma	DQ359349	Irwin et al. (2007)	T1a1'3
Roma	DQ359350	Irwin et al. (2007)	J1c1
Roma	DQ359351	Irwin et al. (2007)	X2b+226
Roma	DQ359352	Irwin et al. (2007)	M5a1
Roma	DQ359353	Irwin et al. (2007)	H5
Roma	DQ359354	Irwin et al. (2007)	X2d1
Roma	DQ359355	Irwin et al. (2007)	X2b+226
Roma	DQ359356	Irwin et al. (2007)	H2a2a
Roma	DQ359357	Irwin et al. (2007)	H55b
Roma	DQ359358	Irwin et al. (2007)	X2d1
Roma	DQ359359	Irwin et al. (2007)	M5a1

Population	GenBank	Reference	Haplogroup (HG)
Roma	DQ359360	Irwin et al. (2007)	M5a1
Roma	DQ359361	Irwin et al. (2007)	H1ao
Roma	DQ359362	Irwin et al. (2007)	M5a1
Roma	DQ359363	Irwin et al. (2007)	H1b1+16362
Roma	DQ359364	Irwin et al. (2007)	H55b
Roma	DQ359365	Irwin et al. (2007)	H1ao
Roma	DQ359366	Irwin et al. (2007)	M35b+16304
Roma	DQ359367	Irwin et al. (2007)	X2d1
Roma	DQ359368	Irwin et al. (2007)	X2b+226
Roma	DQ359369	Irwin et al. (2007)	H5
Roma	DQ359370	Irwin et al. (2007)	X2b+226
Roma	DQ359371	Irwin et al. (2007)	H1ao
Roma	DQ359372	Irwin et al. (2007)	K1c2
Roma	DQ359373	Irwin et al. (2007)	H1ao
Roma	DQ359374	Irwin et al. (2007)	M5a1
Roma	DQ359375	Irwin et al. (2007)	X2d1
Roma	DQ359376	Irwin et al. (2007)	M5a1
Roma	DQ359377	Irwin et al. (2007)	X2d1
Roma	DQ359378	Irwin et al. (2007)	J1c2
Roma	DQ359379	Irwin et al. (2007)	M5a1
Roma	DQ359380	Irwin et al. (2007)	M5a1
Roma	DQ359381	Irwin et al. (2007)	H1e1a4
Roma	DQ359382	Irwin et al. (2007)	M5a1
Roma	DQ359383	Irwin et al. (2007)	M5a1
Roma	DQ359384	Irwin et al. (2007)	X2d1
Roma	DQ359385	Irwin et al. (2007)	M5a1
Roma	DQ359386	Irwin et al. (2007)	H1ao
Roma	DQ359387	Irwin et al. (2007)	M5a1
Roma	DQ359388	Irwin et al. (2007)	HV0
Roma	DQ359389	Irwin et al. (2007)	M35b+16304
Roma	DQ359390	Irwin et al. (2007)	X2b+226
Roma	DQ359391	Irwin et al. (2007)	M5a1
Roma	DQ359392	Irwin et al. (2007)	X2e1b
Roma	DQ359393	Irwin et al. (2007)	X2d1
Roma	DQ359394	Irwin et al. (2007)	N
Roma	DQ359395	Irwin et al. (2007)	N

Population	GenBank	Reference	Haplogroup (HG)
Roma	DQ359396	Irwin et al. (2007)	T2b+16362
Roma	DQ359397	Irwin et al. (2007)	X2b10
Roma	DQ359398	Irwin et al. (2007)	H1ag1a
Roma	DQ359399	Irwin et al. (2007)	X2b+226
Roma	DQ359400	Irwin et al. (2007)	X2b+226
Roma	DQ359401	Irwin et al. (2007)	M5a1
Roma	DQ359402	Irwin et al. (2007)	H2a2a
Roma	DQ359403	Irwin et al. (2007)	U5b2a2
Roma	DQ359404	Irwin et al. (2007)	T2b+16362
Roma	DQ359405	Irwin et al. (2007)	H9a
Roma	DQ359406	Irwin et al. (2007)	M5a1
Roma	DQ359407	Irwin et al. (2007)	H2a+152 16311
Roma	DQ359408	Irwin et al. (2007)	H1b1+16362
Roma	DQ359409	Irwin et al. (2007)	M5a1
Roma	DQ359410	Irwin et al. (2007)	L3f1b
Roma	DQ359411	Irwin et al. (2007)	M5a1
Roma	DQ359412	Irwin et al. (2007)	M5a1
Roma	DQ359413	Irwin et al. (2007)	M5a1
Roma	DQ359414	Irwin et al. (2007)	H1m1
Roma	DQ359415	Irwin et al. (2007)	U5b2a2
Roma	DQ359416	Irwin et al. (2007)	T1a1'3
Roma	DQ359417	Irwin et al. (2007)	X2b+226
Roma	DQ359418	Irwin et al. (2007)	X2b+226
Roma	DQ359419	Irwin et al. (2007)	T1a1'3
Roma	DQ359420	Irwin et al. (2007)	J1
Roma	DQ359421	Irwin et al. (2007)	HV0
Roma	DQ359422	Irwin et al. (2007)	M35b+16304
Roma	DQ359423	Irwin et al. (2007)	M35b+16304
Roma	DQ359424	Irwin et al. (2007)	M5a1
Roma	DQ359425	Irwin et al. (2007)	X2b+226
Roma	DQ359426	Irwin et al. (2007)	U3
Roma	DQ359427	Irwin et al. (2007)	I1a1
Roma	DQ359428	Irwin et al. (2007)	HV0
Roma	DQ359429	Irwin et al. (2007)	N
Roma	DQ359430	Irwin et al. (2007)	M5a1
Roma	DQ359431	Irwin et al. (2007)	M5a1

Population	GenBank	Reference	Haplogroup (HG)
Roma	DQ359432	Irwin et al. (2007)	H6
Roma	DQ359433	Irwin et al. (2007)	H6
Roma	DQ359434	Irwin et al. (2007)	M35b+16304
Roma	DQ359435	Irwin et al. (2007)	X2b+226
Roma	DQ359436	Irwin et al. (2007)	H1a
Roma	DQ359437	Irwin et al. (2007)	M5a1
Roma	DQ359438	Irwin et al. (2007)	X2b+226
Roma	DQ359439	Irwin et al. (2007)	T2b
Roma	DQ359440	Irwin et al. (2007)	U4b1a3
Roma	DQ359441	Irwin et al. (2007)	N
Roma	DQ359442	Irwin et al. (2007)	M5a1
Roma	DQ359443	Irwin et al. (2007)	M5a1
Roma	DQ359444	Irwin et al. (2007)	V+@72
Roma	DQ359445	Irwin et al. (2007)	M5a1
Roma	DQ359446	Irwin et al. (2007)	M5a1
Roma	DQ359447	Irwin et al. (2007)	M5a1
Roma	DQ359448	Irwin et al. (2007)	T2b+16362
Roma	DQ359449	Irwin et al. (2007)	M5a1
Roma	DQ359450	Irwin et al. (2007)	U2d3
Roma	DQ359451	Irwin et al. (2007)	M5a1
Roma	DQ359452	Irwin et al. (2007)	X2b+226
Roma	DQ359453	Irwin et al. (2007)	H1e1a1
Roma	DQ359454	Irwin et al. (2007)	M5a1
Roma	DQ359455	Irwin et al. (2007)	M5a1
Roma	DQ359456	Irwin et al. (2007)	H6
Roma	DQ359457	Irwin et al. (2007)	M5a1
Roma	DQ359458	Irwin et al. (2007)	X2d1
Roma	DQ359459	Irwin et al. (2007)	H1ao
Roma	DQ359460	Irwin et al. (2007)	T2b
Roma	DQ359461	Irwin et al. (2007)	I1a1
Roma	DQ359462	Irwin et al. (2007)	H1b2a
Roma	DQ359463	Irwin et al. (2007)	M5a1
Roma	DQ359464	Irwin et al. (2007)	T2b
Roma	DQ359465	Irwin et al. (2007)	H1m1
Roma	DQ359466	Irwin et al. (2007)	K1c2
Roma	DQ359467	Irwin et al. (2007)	M5a1

Population	GenBank	Reference	Haplogroup (HG)
Roma	DQ359468	Irwin et al. (2007)	M5a1
Roma	DQ359469	Irwin et al. (2007)	T2b
Roma	DQ359470	Irwin et al. (2007)	M5a1
Roma	DQ359471	Irwin et al. (2007)	U5a1a1+152
Roma	DQ359472	Irwin et al. (2007)	H6a1b3
Roma	DQ359473	Irwin et al. (2007)	H6
Roma	DQ359474	Irwin et al. (2007)	T2b+16362
Roma	DQ359475	Irwin et al. (2007)	J1b3a
Roma	DQ359476	Irwin et al. (2007)	H55b
Roma	DQ359477	Irwin et al. (2007)	M5a1
Roma	JQ797790	Pala et al. (2012)	X2d1
Roma	JQ797801	Pala et al. (2012)	U5a1f2
Roma	JQ797807	Pala et al. (2012)	I1a1
Roma	JQ797818	Pala et al. (2012)	M35b+16304
Roma	JQ797849	Pala et al. (2012)	M5a1
Roma	JQ797850	Pala et al. (2012)	H10d
Roma	JQ797853	Pala et al. (2012)	M35b+16304
Roma	JQ797972	Pala et al. (2012)	N
Roma	EU547187	Pala et al. (2012) misc.	X2b+226
Roma	HQ912960	Pala et al. (2012) misc.	M35b+16304
Roma	KC867107	Kushniarevich et al. (2013)	M5a1
Roma	KC867128	Kushniarevich et al. (2013)	T2b+16362
Roma	KP407068	Gandini et al. (unpub)	K1c2
Roma	KP407070	Gandini et al. (unpub)	N
Roma	KP407071	Gandini et al. (unpub)	X2d1
Roma	KP407072	Gandini et al. (unpub)	H1ao
Roma	KP407073	Gandini et al. (unpub)	J1c2
Russia	GU069938	Irwin et al. (2010)	H1+152
Russia	GU069939	Irwin et al. (2010)	U5a1a2
Russia	GU069940	Irwin et al. (2010)	H2a2a1
Russia	GU069941	Irwin et al. (2010)	U4a1
Russia	GU069942	Irwin et al. (2010)	H107
Russia	GU069943	Irwin et al. (2010)	H2a2a
Russia	GU069944	Irwin et al. (2010)	H2a2a
Russia	GU069945	Irwin et al. (2010)	H11a1
Russia	GU069946	Irwin et al. (2010)	U5a2

Population	GenBank	Reference	Haplogroup (HG)
Russia	GU069947	Irwin et al. (2010)	T2b11
Russia	GU069948	Irwin et al. (2010)	H2a1
Russia	GU069949	Irwin et al. (2010)	K1c
Russia	GU069950	Irwin et al. (2010)	H2a2a
Russia	GU069951	Irwin et al. (2010)	H2a2a
Russia	GU069952	Irwin et al. (2010)	H10+(16093)
Russia	GU069953	Irwin et al. (2010)	J1c2
Russia	GU069954	Irwin et al. (2010)	H2a2a
Russia	GU069955	Irwin et al. (2010)	J2b1a6
Russia	GU069956	Irwin et al. (2010)	R1a
Russia	GU069957	Irwin et al. (2010)	K1a4a1a+195
Russia	GU069958	Irwin et al. (2010)	U4a2a
Russia	GU069959	Irwin et al. (2010)	H5a5
Russia	GU069960	Irwin et al. (2010)	U4a2b
Russia	GU069961	Irwin et al. (2010)	X2c
Russia	GU069962	Irwin et al. (2010)	H2a3
Russia	GU069963	Irwin et al. (2010)	HV0a1
Russia	GU069964	Irwin et al. (2010)	H2a+152 16311
Russia	GU069965	Irwin et al. (2010)	T
Russia	GU069966	Irwin et al. (2010)	H2a1
Russia	GU069967	Irwin et al. (2010)	H1c
Russia	GU069968	Irwin et al. (2010)	H1c
Russia	GU069969	Irwin et al. (2010)	U8a1a
Russia	GU069970	Irwin et al. (2010)	U5b1b1+@16192
Russia	GU069971	Irwin et al. (2010)	T2b11
Russia	GU069972	Irwin et al. (2010)	H5a5
Russia	GU069973	Irwin et al. (2010)	I1a1
Russia	GU069974	Irwin et al. (2010)	U8b1a2b
Russia	GU069975	Irwin et al. (2010)	U2e1'2'3
Russia	GU069976	Irwin et al. (2010)	H2a2a
Russia	GU069977	Irwin et al. (2010)	K1c
Russia	GU069978	Irwin et al. (2010)	H1a
Russia	GU069979	Irwin et al. (2010)	H2a2a
Russia	GU069980	Irwin et al. (2010)	H1c
Russia	GU069981	Irwin et al. (2010)	I
Russia	GU069982	Irwin et al. (2010)	H1b1+16362

Population	GenBank	Reference	Haplogroup (HG)
Russia	GU069983	Irwin et al. (2010)	H2a2a
Russia	GU069984	Irwin et al. (2010)	H2a1
Russia	GU069985	Irwin et al. (2010)	H1c
Russia	GU069986	Irwin et al. (2010)	H3h7
Russia	GU069987	Irwin et al. (2010)	U5a1b1d+16093
Russia	GU069988	Irwin et al. (2010)	J2a2a1+16311
Russia	GU069989	Irwin et al. (2010)	HV0
Russia	GU069990	Irwin et al. (2010)	T
Russia	GU069991	Irwin et al. (2010)	H2a2a
Russia	GU069992	Irwin et al. (2010)	H2a2a
Russia	GU069993	Irwin et al. (2010)	J1c2c
Russia	GU069994	Irwin et al. (2010)	V7b
Russia	GU069995	Irwin et al. (2010)	H6
Russia	GU069996	Irwin et al. (2010)	X2d
Russia	GU069997	Irwin et al. (2010)	U5a1+@16192
Russia	GU069998	Irwin et al. (2010)	J1
Russia	GU069999	Irwin et al. (2010)	H13a1b
Russia	GU070000	Irwin et al. (2010)	H2a2a
Russia	GU070001	Irwin et al. (2010)	H2a2a
Russia	GU070002	Irwin et al. (2010)	K1a4a1a+195
Russia	GU070003	Irwin et al. (2010)	U4b1b1b
Russia	GU070004	Irwin et al. (2010)	H2a1
Russia	GU070005	Irwin et al. (2010)	H1c
Russia	GU070006	Irwin et al. (2010)	H2a1
Russia	GU070007	Irwin et al. (2010)	H2a2a
Russia	GU070008	Irwin et al. (2010)	H1+152
Russia	GU070009	Irwin et al. (2010)	U5a1a2
Russia	GU070010	Irwin et al. (2010)	H1bt
Russia	GU070011	Irwin et al. (2010)	T2b
Russia	GU070012	Irwin et al. (2010)	H2a2a
Russia	GU070013	Irwin et al. (2010)	U4a1
Russia	GU070014	Irwin et al. (2010)	H6
Russia	GU070015	Irwin et al. (2010)	J1b1a1
Russia	GU070016	Irwin et al. (2010)	HV1b+152
Russia	GU070017	Irwin et al. (2010)	T1a1'3
Russia	GU070018	Irwin et al. (2010)	H1m1

Population	GenBank	Reference	Haplogroup (HG)
Russia	GU070019	Irwin et al. (2010)	I3a
Russia	GU070020	Irwin et al. (2010)	U2e1'2'3
Russia	GU070021	Irwin et al. (2010)	N1a1a1a
Russia	GU070022	Irwin et al. (2010)	H27+16093
Russia	GU070023	Irwin et al. (2010)	I2a
Russia	GU070024	Irwin et al. (2010)	H1+152
Russia	GU070025	Irwin et al. (2010)	J1c7
Russia	GU070026	Irwin et al. (2010)	H55b
Russia	GU070027	Irwin et al. (2010)	U5b2a1
Russia	GU070028	Irwin et al. (2010)	U4c1
Russia	GU070029	Irwin et al. (2010)	H7c1
Russia	GU070030	Irwin et al. (2010)	K1c
Russia	GU070031	Irwin et al. (2010)	H2a2a
Russia	GU070032	Irwin et al. (2010)	W6
Russia	GU070033	Irwin et al. (2010)	H6
Russia	GU070034	Irwin et al. (2010)	U5a2b1b
Russia	GU070035	Irwin et al. (2010)	K1b2
Russia	GU070036	Irwin et al. (2010)	J1c
Russia	GU070037	Irwin et al. (2010)	H1b
Russia	GU070038	Irwin et al. (2010)	W3a1+199
Russia	GU070039	Irwin et al. (2010)	H2a2a1
Russia	GU070040	Irwin et al. (2010)	H11a1
Russia	GU070041	Irwin et al. (2010)	J1
Russia	GU070042	Irwin et al. (2010)	H11
Russia	GU070043	Irwin et al. (2010)	H2a1
Russia	GU070044	Irwin et al. (2010)	HV9b
Russia	GU070045	Irwin et al. (2010)	HV0a1
Russia	GU070046	Irwin et al. (2010)	T2b
Russia	GU070047	Irwin et al. (2010)	V7a
Russia	GU070048	Irwin et al. (2010)	HV0a1
Russia	GU070049	Irwin et al. (2010)	U5a2
Russia	GU070050	Irwin et al. (2010)	H1e5
Russia	GU070051	Irwin et al. (2010)	H1b1+16362
Russia	GU070052	Irwin et al. (2010)	H28
Russia	GU070053	Irwin et al. (2010)	H2a1
Russia	GU070054	Irwin et al. (2010)	W6

Population	GenBank	Reference	Haplogroup (HG)
Russia	GU070055	Irwin et al. (2010)	J1c2
Russia	GU070056	Irwin et al. (2010)	T2a1b
Russia	GU070057	Irwin et al. (2010)	U5b
Russia	GU070058	Irwin et al. (2010)	H7i
Russia	GU070059	Irwin et al. (2010)	H11a2a2
Russia	GU070060	Irwin et al. (2010)	V+@72
Russia	GU070061	Irwin et al. (2010)	U3
Russia	GU070062	Irwin et al. (2010)	U5b1e
Russia	GU070063	Irwin et al. (2010)	H2a5b1
Russia	GU070064	Irwin et al. (2010)	HV9b
Russia	GU070065	Irwin et al. (2010)	H1b3
Russia	GU070066	Irwin et al. (2010)	H2a2a
Russia	GU070067	Irwin et al. (2010)	V7a
Russia	GU070068	Irwin et al. (2010)	T1a
Russia	GU070069	Irwin et al. (2010)	U5a1d2b
Russia	GU070070	Irwin et al. (2010)	H2a1+146
Russia	GU070071	Irwin et al. (2010)	H1c+152
Russia	GU070072	Irwin et al. (2010)	H5
Russia	GU070073	Irwin et al. (2010)	V7
Russia	GU070074	Irwin et al. (2010)	H1b1+16362
Russia	GU070075	Irwin et al. (2010)	H5
Russia	GU070076	Irwin et al. (2010)	H5
Russia	GU070077	Irwin et al. (2010)	H7c1
Russia	GU070078	Irwin et al. (2010)	U5a2
Russia	GU070079	Irwin et al. (2010)	U5a1b1c2
Russia	GU070080	Irwin et al. (2010)	H5
Russia	GU070081	Irwin et al. (2010)	H6
Russia	GU070082	Irwin et al. (2010)	U3
Russia	GU070083	Irwin et al. (2010)	K1a4a1a+195
Russia	GU070084	Irwin et al. (2010)	U2e1
Russia	GU070085	Irwin et al. (2010)	H39
Russia	GU070086	Irwin et al. (2010)	V7a
Russia	GU070087	Irwin et al. (2010)	H5
Russia	GU070088	Irwin et al. (2010)	T2
Saudi Arabia	JQ798046	Pala et al. (2012)	T1b
Saudi Arabia	DQ301817	Behar et al. (2006)	K1a8

Population	GenBank	Reference	Haplogroup (HG)
Saudi Arabia	KC867116	Kushniarevich et al. (2013)	N1a3a
Saudi Arabia	KC867117	Kushniarevich et al. (2013)	N1a3a
Saudi Arabia	KC152593	Pennarun et al. (2012)	M1a1b1b1
Saudi Arabia	KC152594	Pennarun et al. (2012)	M1a1f
Saudi Arabia	DQ904234	Abu-Amero et al. (2006)	M14
Saudi Arabia	DQ904235	Abu-Amero et al. (2006)	R0a1a
Saudi Arabia	DQ904236	Abu-Amero et al. (2006)	R0a1b
Saudi Arabia	DQ904237	Abu-Amero et al. (2006)	R0a1a
Saudi Arabia	DQ904238	Abu-Amero et al. (2006)	R0a2c
Saudi Arabia	DQ904239	Abu-Amero et al. (2006)	R0a1a
Saudi Arabia	DQ904240	Abu-Amero et al. (2006)	R0a2h
Saudi Arabia	DQ904241	Abu-Amero et al. (2006)	R0a2i
Saudi Arabia	EU370392	Abu-Amero et al. (2008)	M1a4
Saudi Arabia	EU370393	Abu-Amero et al. (2008)	M33a
Saudi Arabia	EU370394	Abu-Amero et al. (2008)	M36a
Saudi Arabia	EU370395	Abu-Amero et al. (2008)	M48
Shor	JN857060	Derenko et al. (2012)	M10a1*
Shor	JN857059	Derenko et al. (2012)	B4b1a3a1a
Shor	FJ951607	Derenko et al. (2010)	C4a1a1
Shor	FJ951608	Derenko et al. (2010)	C4a2a1
Shor	FJ951609	Derenko et al. (2010)	C4a2a1
Shor	FJ951610	Derenko et al. (2010)	C4d
Shor	EU007883	Ingman and Gyllensten (2007)	D4f
Shor	EU007882	Ingman and Gyllensten (2007)	H8b1
Shor	EU007881	Ingman and Gyllensten (2007)	D5c1a
Shor	KJ856683	Derenko et al. (2014)	U4b1b1c
Shor	KJ856764	Derenko et al. (2014)	H8b1b
Shor	KJ856780	Derenko et al. (2014)	H6a1b
Slovakia	JQ797963	Pala et al. (2012)	J2b1
Slovakia	JX307099	Mielnik-Sikorska et al. (2013)	H6c1
Slovakia	JX307100	Mielnik-Sikorska et al. (2013)	H6a1a
Slovakia	JX307109	Mielnik-Sikorska et al. (2013)	H6a1a
Slovakia	JX128071	Mielnik-Sikorska et al. (2013)	H5a1g1
Slovakia	JX128072	Mielnik-Sikorska et al. (2013)	H5a1a
Slovakia	JX128073	Mielnik-Sikorska et al. (2013)	H5m
Slovakia	JX128074	Mielnik-Sikorska et al. (2013)	H5a1a

Population	GenBank	Reference	Haplogroup (HG)
Slovakia	JX128075	Mielnik-Sikorska et al. (2013)	H5b1
Slovakia	JX128076	Mielnik-Sikorska et al. (2013)	H5a1f
Slovakia	JX128077	Mielnik-Sikorska et al. (2013)	H5a1+152
Slovakia	JX128078	Mielnik-Sikorska et al. (2013)	H5a2
Slovakia	EU200763	Malyarchuk et al. (2008)	L2a1a
Slovakia	EU200762	Malyarchuk et al. (2008)	L2a1
Slovakia	EU545463.3	Malyarchuk et al. (2008a)	U4b
Slovakia	EU545462.3	Malyarchuk et al. (2008a)	U4c
Slovakia	EU545461.3	Malyarchuk et al. (2008a)	U4a2
Slovakia	EU545460.3	Malyarchuk et al. (2008a)	U4c
Slovakia	EU545459.3	Malyarchuk et al. (2008a)	U4a1
Slovakia	EU545458.3	Malyarchuk et al. (2008a)	U4a2
Syria	JQ797949	Pala et al. (2012)	J2b1
Syria	JQ797959	Pala et al. (2012)	J2b1d1
Syria	JQ797968	Pala et al. (2012)	J2b1f
Syria	DQ301818	Behar et al. (2006)	K1a8
Syria	KP407030	Gandini et al. (unpub)	R0a1a7
Syria	JQ706061	Behar et al. (2012)	K1a
Szekely	EF185603	Brandstatter et al. (2007)	H13a2c
Szekely	EF185604	Brandstatter et al. (2007)	U2e1
Szekely	EF185605	Brandstatter et al. (2007)	W+194
Szekely	EF185606	Brandstatter et al. (2007)	H2a5b1
Szekely	EF185607	Brandstatter et al. (2007)	H2a2a
Szekely	EF185608	Brandstatter et al. (2007)	X2+225+@16223
Szekely	EF185609	Brandstatter et al. (2007)	H14b1
Szekely	EF185610	Brandstatter et al. (2007)	U7a
Szekely	EF185611	Brandstatter et al. (2007)	W1e1a
Szekely	EF185612	Brandstatter et al. (2007)	N
Szekely	EF185613	Brandstatter et al. (2007)	W+194
Szekely	EF185614	Brandstatter et al. (2007)	C5c+16234
Szekely	EF185615	Brandstatter et al. (2007)	C4e
Szekely	EF185616	Brandstatter et al. (2007)	H76a
Szekely	EF185617	Brandstatter et al. (2007)	H13a1a2a
Szekely	EF185618	Brandstatter et al. (2007)	H1e1a+16278
Szekely	EF185619	Brandstatter et al. (2007)	H2a+152 16311
Szekely	EF185620	Brandstatter et al. (2007)	U8a

Population	GenBank	Reference	Haplogroup (HG)
Szekely	EF185621	Brandstatter et al. (2007)	HV0
Szekely	EF185622	Brandstatter et al. (2007)	U5b1c1a
Szekely	EF185623	Brandstatter et al. (2007)	R0+16189
Szekely	EF185624	Brandstatter et al. (2007)	U5b1c2
Szekely	EF185625	Brandstatter et al. (2007)	H1b1+16362
Szekely	EF185626	Brandstatter et al. (2007)	X2
Szekely	EF185627	Brandstatter et al. (2007)	J1c2r
Szekely	EF185628	Brandstatter et al. (2007)	T1a1'3
Szekely	EF185629	Brandstatter et al. (2007)	W3a1+199
Szekely	EF185630	Brandstatter et al. (2007)	J2a1a1a
Szekely	EF185631	Brandstatter et al. (2007)	C4e
Szekely	EF185632	Brandstatter et al. (2007)	V+@72
Szekely	EF185633	Brandstatter et al. (2007)	R0+16189
Szekely	EF185634	Brandstatter et al. (2007)	C4a1a+195
Szekely	EF185635	Brandstatter et al. (2007)	U5a1+@16192
Szekely	EF185636	Brandstatter et al. (2007)	H1+152
Szekely	EF185637	Brandstatter et al. (2007)	U8a1a
Szekely	EF185638	Brandstatter et al. (2007)	H1+16189
Szekely	EF185639	Brandstatter et al. (2007)	H7a1a
Szekely	EF185640	Brandstatter et al. (2007)	U4c1
Szekely	EF185641	Brandstatter et al. (2007)	H5
Szekely	EF185642	Brandstatter et al. (2007)	J1c2
Szekely	EF185643	Brandstatter et al. (2007)	H1e1a5
Szekely	EF185644	Brandstatter et al. (2007)	H11
Szekely	EF185645	Brandstatter et al. (2007)	H24
Szekely	EF185646	Brandstatter et al. (2007)	J1
Szekely	EF185647	Brandstatter et al. (2007)	C4a1a+195
Szekely	EF185648	Brandstatter et al. (2007)	U2e2
Szekely	EF185649	Brandstatter et al. (2007)	W
Szekely	EF185650	Brandstatter et al. (2007)	H1+16239
Szekely	EF185651	Brandstatter et al. (2007)	T2c1a
Szekely	EF185652	Brandstatter et al. (2007)	R0a1a
Szekely	EF185653	Brandstatter et al. (2007)	K1a11
Szekely	EF185654	Brandstatter et al. (2007)	J1c
Szekely	EF185655	Brandstatter et al. (2007)	HV0
Szekely	EF185656	Brandstatter et al. (2007)	T2b

Population	GenBank	Reference	Haplogroup (HG)
Szekely	EF185657	Brandstatter et al. (2007)	Y1
Szekely	EF185658	Brandstatter et al. (2007)	H6
Szekely	EF185659	Brandstatter et al. (2007)	U4
Szekely	EF185660	Brandstatter et al. (2007)	H2a2a
Szekely	EF185661	Brandstatter et al. (2007)	H1+16239
Szekely	EF185662	Brandstatter et al. (2007)	H1b1b
Szekely	EF185663	Brandstatter et al. (2007)	B4c1a2
Szekely	EF185664	Brandstatter et al. (2007)	J1c2o
Szekely	EF185665	Brandstatter et al. (2007)	H1ap1
Szekely	EF185666	Brandstatter et al. (2007)	H14b1
Szekely	EF185667	Brandstatter et al. (2007)	H5
Szekely	EF185668	Brandstatter et al. (2007)	H5a4
Szekely	EF185669	Brandstatter et al. (2007)	H5
Szekely	EF185670	Brandstatter et al. (2007)	U4a1
Szekely	EF185671	Brandstatter et al. (2007)	H1e1a4
Szekely	EF185672	Brandstatter et al. (2007)	H14b1
Szekely	EF185673	Brandstatter et al. (2007)	H1c
Szekely	EF185674	Brandstatter et al. (2007)	H13a2c
Szekely	EF185675	Brandstatter et al. (2007)	X2d1
Szekely	EF185676	Brandstatter et al. (2007)	H2a2a
Szekely	EF185677	Brandstatter et al. (2007)	U5a1+@16192
Szekely	EF185678	Brandstatter et al. (2007)	HV0
Szekely	EF185679	Brandstatter et al. (2007)	T1a1'3
Szekely	EF185680	Brandstatter et al. (2007)	H1b1b
Szekely	EF185681	Brandstatter et al. (2007)	J1b
Szekely	EF185682	Brandstatter et al. (2007)	U5b2a2
Szekely	EF185683	Brandstatter et al. (2007)	H1ao
Szekely	EF185684	Brandstatter et al. (2007)	HV0
Szekely	EF185685	Brandstatter et al. (2007)	U5a1b1
Szekely	EF185686	Brandstatter et al. (2007)	U5b2a1a+16311
Szekely	EF185687	Brandstatter et al. (2007)	H5+16192
Szekely	EF185688	Brandstatter et al. (2007)	T2b24
Szekely	EF185689	Brandstatter et al. (2007)	HV0+195
Szekely	EF185690	Brandstatter et al. (2007)	R0a1a
Szekely	EF185691	Brandstatter et al. (2007)	H2a2a
Szekely	EF185692	Brandstatter et al. (2007)	J1c1

Population	GenBank	Reference	Haplogroup (HG)
Szekely	EF185693	Brandstatter et al. (2007)	G2a
Szekely	EF185694	Brandstatter et al. (2007)	K1c
Szekely	EF185695	Brandstatter et al. (2007)	W+194
Szekely	EF185696	Brandstatter et al. (2007)	C5c+16234
Szekely	EF185697	Brandstatter et al. (2007)	H66a
Szekely	EF185698	Brandstatter et al. (2007)	H1b1b
Szekely	EF185699	Brandstatter et al. (2007)	K1a2a1
Szekely	EF185700	Brandstatter et al. (2007)	H2a2a
Szekely	EF185701	Brandstatter et al. (2007)	K1b1+(16093)
Szekely	EF185702	Brandstatter et al. (2007)	U5b
Szekely	EF185703	Brandstatter et al. (2007)	A8a1
Szekely	EF185704	Brandstatter et al. (2007)	T2
Szekely	EF185705	Brandstatter et al. (2007)	H27
Szekely	EF185706	Brandstatter et al. (2007)	J1c
Szekely	EF185707	Brandstatter et al. (2007)	H1c
Szekely	EF185708	Brandstatter et al. (2007)	U5a1b1
Szekely	EF185709	Brandstatter et al. (2007)	X2+225+@16223
Szekely	EF185710	Brandstatter et al. (2007)	H66a
Szekely	EF185711	Brandstatter et al. (2007)	T2b4+152
Szekely	EF185712	Brandstatter et al. (2007)	W1e1a
Szekely	EF185713	Brandstatter et al. (2007)	H10g
Szekely	EF185714	Brandstatter et al. (2007)	T2g1
Szekely	EF185715	Brandstatter et al. (2007)	J1c2
Szekely	EF185716	Brandstatter et al. (2007)	U1a1a
Szekely	EF185717	Brandstatter et al. (2007)	H6
Szekely	EF185718	Brandstatter et al. (2007)	U5a2e
Szekely	EF185719	Brandstatter et al. (2007)	U2d3
Szekely	EF185720	Brandstatter et al. (2007)	H5a4
Szekely	EF185721	Brandstatter et al. (2007)	W3a1+199
Szekely	EF185722	Brandstatter et al. (2007)	T2b
Szekely	EF185723	Brandstatter et al. (2007)	J1
Szekely	EF185724	Brandstatter et al. (2007)	V9
Szekely	EF185725	Brandstatter et al. (2007)	U8a1a
Szekely	EF185726	Brandstatter et al. (2007)	H1b1+16362
Szekely	EF185727	Brandstatter et al. (2007)	U4c1
Szekely	EF185728	Brandstatter et al. (2007)	T2f1a

Population	GenBank	Reference	Haplogroup (HG)
Szekely	EF185729	Brandstatter et al. (2007)	T2b3+151
Szekely	EF185730	Brandstatter et al. (2007)	H66a
Szekely	EF185731	Brandstatter et al. (2007)	C5b1
Szekely	EF185732	Brandstatter et al. (2007)	U8a1a
Szekely	EF185733	Brandstatter et al. (2007)	U4
Szekely	EF185734	Brandstatter et al. (2007)	U8a1a
Szekely	EF185735	Brandstatter et al. (2007)	J1c2e
Szekely	EF185736	Brandstatter et al. (2007)	H1e+16129
Szekely	EF185737	Brandstatter et al. (2007)	K1a4a1a+195
Szekely	EF185738	Brandstatter et al. (2007)	C4a1a+195
Szekely	EF185739	Brandstatter et al. (2007)	H14b2a
Szekely	EF185740	Brandstatter et al. (2007)	U5b1b1a
Szekely	EF185741	Brandstatter et al. (2007)	I1a1
Szekely	EF185742	Brandstatter et al. (2007)	H2a2a
Szekely	EF185743	Brandstatter et al. (2007)	W
Szekely	EF185744	Brandstatter et al. (2007)	T2b3e
Szekely	EF185745	Brandstatter et al. (2007)	K1a5a
Szekely	EF185746	Brandstatter et al. (2007)	J1b1a
Szekely	EF185747	Brandstatter et al. (2007)	U5a1
Szekely	EF185748	Brandstatter et al. (2007)	H5b4
Szekely	EF185749	Brandstatter et al. (2007)	H1c
Szekely	EF185750	Brandstatter et al. (2007)	H66a
Szekely	EF185751	Brandstatter et al. (2007)	U4a1
Szekely	EF185752	Brandstatter et al. (2007)	C5b1
Szekely	EF185753	Brandstatter et al. (2007)	K1a4c1
Szekely	EF185754	Brandstatter et al. (2007)	N1b1
Szekely	EF185755	Brandstatter et al. (2007)	T1a1'3
Szekely	EF185756	Brandstatter et al. (2007)	J1c2e
Szekely	EF185757	Brandstatter et al. (2007)	H5a4
Szekely	EF185758	Brandstatter et al. (2007)	H1q3
Szekely	EF185759	Brandstatter et al. (2007)	H66a
Szekely	EF185760	Brandstatter et al. (2007)	U5b1b1+@16192
Szekely	EF185761	Brandstatter et al. (2007)	T2b
Szekely	EF185762	Brandstatter et al. (2007)	A8a1
Szekely	EF185763	Brandstatter et al. (2007)	T1a+152
Szekely	EF185764	Brandstatter et al. (2007)	H66a

Population	GenBank	Reference	Haplogroup (HG)
Szekely	EF185765	Brandstatter et al. (2007)	H2a2a
Szekely	EF185766	Brandstatter et al. (2007)	K1a
Szekely	EF185767	Brandstatter et al. (2007)	H5
Szekely	EF185768	Brandstatter et al. (2007)	H2a2a
Szekely	EF185769	Brandstatter et al. (2007)	H66a
Szekely	EF185770	Brandstatter et al. (2007)	H1c
Szekely	EF185771	Brandstatter et al. (2007)	HV1b+152
Szekely	EF185772	Brandstatter et al. (2007)	V+@72
Szekely	EF185773	Brandstatter et al. (2007)	T2f1a
Szekely	EF185774	Brandstatter et al. (2007)	H5
Szekely	EF185775	Brandstatter et al. (2007)	T2a1b
Szekely	EF185776	Brandstatter et al. (2007)	HV0
Szekely	EF185777	Brandstatter et al. (2007)	U1a1a
Szekely	EF185778	Brandstatter et al. (2007)	J1c2r
Szekely	EF185779	Brandstatter et al. (2007)	U8b1a1
Szekely	EF185780	Brandstatter et al. (2007)	U5b
Tajikistan	GU070089	Irwin et al. (2010)	M30c1
Tajikistan	GU070090	Irwin et al. (2010)	F1b1+@152
Tajikistan	GU070091	Irwin et al. (2010)	T2g1b
Tajikistan	GU070092	Irwin et al. (2010)	F1b1b
Tajikistan	GU070093	Irwin et al. (2010)	D5c1a
Tajikistan	GU070094	Irwin et al. (2010)	U7a4
Tajikistan	GU070095	Irwin et al. (2010)	T1a1'3
Tajikistan	GU070096	Irwin et al. (2010)	HV14
Tajikistan	GU070097	Irwin et al. (2010)	HV14
Tajikistan	GU070098	Irwin et al. (2010)	H6b
Tajikistan	GU070099	Irwin et al. (2010)	H5
Tajikistan	GU070100	Irwin et al. (2010)	T1a1m
Tajikistan	GU070101	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070102	Irwin et al. (2010)	U1a
Tajikistan	GU070103	Irwin et al. (2010)	H15a1a1
Tajikistan	GU070104	Irwin et al. (2010)	K1a+150
Tajikistan	GU070105	Irwin et al. (2010)	R1b
Tajikistan	GU070106	Irwin et al. (2010)	U3b3
Tajikistan	GU070107	Irwin et al. (2010)	W
Tajikistan	GU070108	Irwin et al. (2010)	D4b2a2a

Population	GenBank	Reference	Haplogroup (HG)
Tajikistan	GU070109	Irwin et al. (2010)	H15a1a1
Tajikistan	GU070110	Irwin et al. (2010)	F1b1+@152
Tajikistan	GU070111	Irwin et al. (2010)	W
Tajikistan	GU070112	Irwin et al. (2010)	U7a
Tajikistan	GU070113	Irwin et al. (2010)	H14a
Tajikistan	GU070114	Irwin et al. (2010)	C5b1
Tajikistan	GU070115	Irwin et al. (2010)	B4b1a1c
Tajikistan	GU070116	Irwin et al. (2010)	U3a
Tajikistan	GU070117	Irwin et al. (2010)	W
Tajikistan	GU070118	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070119	Irwin et al. (2010)	M11
Tajikistan	GU070120	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070121	Irwin et al. (2010)	T2d1
Tajikistan	GU070122	Irwin et al. (2010)	T2d1
Tajikistan	GU070123	Irwin et al. (2010)	U7a4
Tajikistan	GU070124	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070125	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070126	Irwin et al. (2010)	D4b2b
Tajikistan	GU070127	Irwin et al. (2010)	F1b1+@152
Tajikistan	GU070128	Irwin et al. (2010)	D4b2a2a
Tajikistan	GU070129	Irwin et al. (2010)	C4b3
Tajikistan	GU070130	Irwin et al. (2010)	F
Tajikistan	GU070131	Irwin et al. (2010)	N1a2
Tajikistan	GU070132	Irwin et al. (2010)	HV14
Tajikistan	GU070133	Irwin et al. (2010)	W
Tajikistan	GU070134	Irwin et al. (2010)	H15a1a1
Tajikistan	GU070135	Irwin et al. (2010)	U5a1+@16192
Tajikistan	GU070136	Irwin et al. (2010)	U5b1c2
Tajikistan	GU070137	Irwin et al. (2010)	H15a1a1
Tajikistan	GU070138	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070139	Irwin et al. (2010)	C4b3
Tajikistan	GU070140	Irwin et al. (2010)	H15a1a1
Tajikistan	GU070141	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070142	Irwin et al. (2010)	D5c1a
Tajikistan	GU070143	Irwin et al. (2010)	U5a1+@16192
Tajikistan	GU070144	Irwin et al. (2010)	F

Population	GenBank	Reference	Haplogroup (HG)
Tajikistan	GU070145	Irwin et al. (2010)	F
Tajikistan	GU070146	Irwin et al. (2010)	H1n+146+195
Tajikistan	GU070147	Irwin et al. (2010)	U7a4
Tajikistan	GU070148	Irwin et al. (2010)	W
Tajikistan	GU070149	Irwin et al. (2010)	F1b1b
Tajikistan	GU070150	Irwin et al. (2010)	M33a1b
Tajikistan	GU070151	Irwin et al. (2010)	T1a
Tajikistan	GU070152	Irwin et al. (2010)	U5b1c2
Tajikistan	GU070153	Irwin et al. (2010)	M7c1a1b
Tajikistan	GU070154	Irwin et al. (2010)	T2d1
Tajikistan	GU070155	Irwin et al. (2010)	J1b7
Tajikistan	GU070156	Irwin et al. (2010)	H2a5a1
Tajikistan	GU070157	Irwin et al. (2010)	R9
Tajikistan	GU070158	Irwin et al. (2010)	M11+200
Tajikistan	GU070159	Irwin et al. (2010)	U5a1+@16192
Tajikistan	GU070160	Irwin et al. (2010)	T1a1'3
Tajikistan	GU070161	Irwin et al. (2010)	D5c1a
Tajikistan	GU070162	Irwin et al. (2010)	U2e2
Tajikistan	GU070163	Irwin et al. (2010)	H1n+146+195
Tajikistan	GU070164	Irwin et al. (2010)	F1b1+@152
Tajikistan	GU070165	Irwin et al. (2010)	U5a1+@16192
Tajikistan	GU070166	Irwin et al. (2010)	D4b2a2a
Tajikistan	GU070167	Irwin et al. (2010)	D4a+16294
Tajikistan	GU070168	Irwin et al. (2010)	C4e
Tajikistan	GU070169	Irwin et al. (2010)	U5a1+@16192
Tajikistan	GU070170	Irwin et al. (2010)	H5
Tajikistan	GU070171	Irwin et al. (2010)	H5
Tajikistan	GU070172	Irwin et al. (2010)	D4b2a2a
Tajikistan	GU070173	Irwin et al. (2010)	W
Tajikistan	GU070174	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070175	Irwin et al. (2010)	U1a
Tajikistan	GU070176	Irwin et al. (2010)	U3a
Tajikistan	GU070177	Irwin et al. (2010)	F1b1+@152
Tajikistan	GU070178	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070179	Irwin et al. (2010)	D4b2a2a
Tajikistan	GU070180	Irwin et al. (2010)	D5c1a

Population	GenBank	Reference	Haplogroup (HG)
Tajikistan	GU070181	Irwin et al. (2010)	U3a
Tajikistan	GU070182	Irwin et al. (2010)	C4b3
Tajikistan	GU070183	Irwin et al. (2010)	W
Tajikistan	GU070184	Irwin et al. (2010)	F1b1+@152
Tajikistan	GU070185	Irwin et al. (2010)	H15a1a1
Tajikistan	GU070186	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070187	Irwin et al. (2010)	W
Tajikistan	GU070188	Irwin et al. (2010)	T1a1'3
Tajikistan	GU070189	Irwin et al. (2010)	H6b
Tajikistan	GU070190	Irwin et al. (2010)	U7a
Tajikistan	GU070191	Irwin et al. (2010)	H5
Tajikistan	GU070192	Irwin et al. (2010)	U5a1+@16192
Tajikistan	GU070193	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070194	Irwin et al. (2010)	T1a1'3
Tajikistan	GU070195	Irwin et al. (2010)	M65a+@16311
Tajikistan	GU070196	Irwin et al. (2010)	D4b2a2a
Tajikistan	GU070197	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070198	Irwin et al. (2010)	U5a1+@16192
Tajikistan	GU070199	Irwin et al. (2010)	U3a
Tajikistan	GU070200	Irwin et al. (2010)	W
Tajikistan	GU070201	Irwin et al. (2010)	U5a1+@16192
Tajikistan	GU070202	Irwin et al. (2010)	T1a1'3
Tajikistan	GU070203	Irwin et al. (2010)	T1a1m
Tajikistan	GU070204	Irwin et al. (2010)	F1b1+@152
Tajikistan	GU070205	Irwin et al. (2010)	T2d1
Tajikistan	GU070206	Irwin et al. (2010)	H5
Tajikistan	GU070207	Irwin et al. (2010)	F
Tajikistan	GU070208	Irwin et al. (2010)	W
Tajikistan	GU070209	Irwin et al. (2010)	U7a4
Tajikistan	GU070210	Irwin et al. (2010)	K1a+150
Tajikistan	GU070211	Irwin et al. (2010)	C4b3
Tajikistan	GU070212	Irwin et al. (2010)	U1a1a+16129
Tajikistan	GU070213	Irwin et al. (2010)	HV1a1
Tajikistan	GU070214	Irwin et al. (2010)	U5a1+@16192
Tajikistan	GU070215	Irwin et al. (2010)	W
Tajikistan	GU070216	Irwin et al. (2010)	F1b1+@152

Population	GenBank	Reference	Haplogroup (HG)
Tajikistan	GU070217	Irwin et al. (2010)	W
Tajikistan	GU070218	Irwin et al. (2010)	F1b1+@152
Tajikistan	GU070219	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070220	Irwin et al. (2010)	H2a5a1
Tajikistan	GU070221	Irwin et al. (2010)	F1b1+@152
Tajikistan	GU070222	Irwin et al. (2010)	U1a
Tajikistan	GU070223	Irwin et al. (2010)	D5c1a
Tajikistan	GU070224	Irwin et al. (2010)	U1a
Tajikistan	GU070225	Irwin et al. (2010)	K1a+150
Tajikistan	GU070226	Irwin et al. (2010)	U5a1+@16192
Tajikistan	GU070227	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070228	Irwin et al. (2010)	F1b1+@152
Tajikistan	GU070229	Irwin et al. (2010)	D4e2a
Tajikistan	GU070230	Irwin et al. (2010)	U1a
Tajikistan	GU070231	Irwin et al. (2010)	D4e2a
Tajikistan	GU070232	Irwin et al. (2010)	U5a1+@16192
Tajikistan	GU070233	Irwin et al. (2010)	U5b1c2
Tajikistan	GU070234	Irwin et al. (2010)	M45
Tajikistan	GU070235	Irwin et al. (2010)	U1a
Tajikistan	GU070236	Irwin et al. (2010)	U2e2
Tajikistan	GU070237	Irwin et al. (2010)	HV6
Tajikistan	GU070238	Irwin et al. (2010)	D5c1a
Tajikistan	GU070239	Irwin et al. (2010)	U5a1a1+152
Tajikistan	GU070240	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070241	Irwin et al. (2010)	D5c1a
Tajikistan	GU070242	Irwin et al. (2010)	U5b1c2
Tajikistan	GU070243	Irwin et al. (2010)	D4e2a
Tajikistan	GU070244	Irwin et al. (2010)	H1e1a1
Tajikistan	GU070245	Irwin et al. (2010)	T2d1
Tajikistan	GU070246	Irwin et al. (2010)	D4e2a
Tajikistan	GU070247	Irwin et al. (2010)	F1b1+@152
Tajikistan	GU070248	Irwin et al. (2010)	M10
Tajikistan	GU070249	Irwin et al. (2010)	F1b1+@152
Tajikistan	GU070250	Irwin et al. (2010)	T1a1'3
Tajikistan	GU070251	Irwin et al. (2010)	J1b3
Tajikistan	GU070252	Irwin et al. (2010)	W

Population	GenBank	Reference	Haplogroup (HG)
Tajikistan	GU070253	Irwin et al. (2010)	M10
Tajikistan	GU070254	Irwin et al. (2010)	F1b1+@152
Tajikistan	GU070255	Irwin et al. (2010)	T1a1'3
Tajikistan	GU070256	Irwin et al. (2010)	G2a5
Tajikistan	GU070257	Irwin et al. (2010)	D5c1a
Tajikistan	GU070258	Irwin et al. (2010)	D5c1a
Tajikistan	GU070259	Irwin et al. (2010)	U7a4
Tajikistan	GU070260	Irwin et al. (2010)	U5a1a1+152
Tajikistan	GU070261	Irwin et al. (2010)	U7a
Tajikistan	GU070262	Irwin et al. (2010)	F
Tajikistan	GU070263	Irwin et al. (2010)	H15a1a1
Tajikistan	GU070264	Irwin et al. (2010)	U5a1+@16192
Tajikistan	GU070265	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070266	Irwin et al. (2010)	F
Tajikistan	GU070267	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070268	Irwin et al. (2010)	F1b1b
Tajikistan	GU070269	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070270	Irwin et al. (2010)	U7a4
Tajikistan	GU070271	Irwin et al. (2010)	F1b1+@152
Tajikistan	GU070272	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070273	Irwin et al. (2010)	F1b1+@152
Tajikistan	GU070274	Irwin et al. (2010)	H2a5a1
Tajikistan	GU070275	Irwin et al. (2010)	U5a1+@16192
Tajikistan	GU070276	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070277	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070278	Irwin et al. (2010)	T1a13
Tajikistan	GU070279	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070280	Irwin et al. (2010)	M10
Tajikistan	GU070281	Irwin et al. (2010)	J1c
Tajikistan	GU070282	Irwin et al. (2010)	H15a1a1
Tajikistan	GU070283	Irwin et al. (2010)	H15a1a1
Tajikistan	GU070284	Irwin et al. (2010)	M7c1a1b
Tajikistan	GU070285	Irwin et al. (2010)	N1a2
Tajikistan	GU070286	Irwin et al. (2010)	D4e2a
Tajikistan	GU070287	Irwin et al. (2010)	U2e2
Tajikistan	GU070288	Irwin et al. (2010)	U2e2

Population	GenBank	Reference	Haplogroup (HG)
Tajikistan	GU070289	Irwin et al. (2010)	M33a1b
Tajikistan	GU070290	Irwin et al. (2010)	H15a1a1
Tajikistan	GU070291	Irwin et al. (2010)	D5c1a
Tajikistan	GU070292	Irwin et al. (2010)	F1b1+@152
Tajikistan	GU070293	Irwin et al. (2010)	A+152+16362
Tajikistan	GU070294	Irwin et al. (2010)	W
Tajikistan	GU070295	Irwin et al. (2010)	F1b1+@152
Tajikistan	GU070296	Irwin et al. (2010)	T1a1'3
Tajikistan	GU070297	Irwin et al. (2010)	U5a1a1+152
Tajikistan	GU070298	Irwin et al. (2010)	F1b1b
Tajikistan	GU070299	Irwin et al. (2010)	U7a4
Tajikistan	GU070300	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070301	Irwin et al. (2010)	M33a1b
Tajikistan	GU070302	Irwin et al. (2010)	H15a1a1
Tajikistan	GU070303	Irwin et al. (2010)	M7c1a1b
Tajikistan	GU070304	Irwin et al. (2010)	F1b1+@152
Tajikistan	GU070305	Irwin et al. (2010)	T1
Tajikistan	GU070306	Irwin et al. (2010)	U5a1a1+152
Tajikistan	GU070307	Irwin et al. (2010)	N1b1
Tajikistan	GU070308	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070309	Irwin et al. (2010)	D4e2a
Tajikistan	GU070310	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070311	Irwin et al. (2010)	U1a
Tajikistan	GU070312	Irwin et al. (2010)	C4b3
Tajikistan	GU070313	Irwin et al. (2010)	C4b1
Tajikistan	GU070314	Irwin et al. (2010)	A+152+16362
Tajikistan	GU070315	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070316	Irwin et al. (2010)	U5a1+@16192
Tajikistan	GU070317	Irwin et al. (2010)	A+152+16362
Tajikistan	GU070318	Irwin et al. (2010)	H2a2a1
Tajikistan	GU070319	Irwin et al. (2010)	U2e1'2'3
Tajikistan	GU070320	Irwin et al. (2010)	H2a5a1
Tajikistan	GU070321	Irwin et al. (2010)	U7a4
Tajikistan	GU070322	Irwin et al. (2010)	M30+16234
Tajikistan	GU070323	Irwin et al. (2010)	A+152+16362
Tajikistan	GU070324	Irwin et al. (2010)	C4a1a+195

Population	GenBank	Reference	Haplogroup (HG)
Tajikistan	GU070325	Irwin et al. (2010)	M33a1b
Tajikistan	GU070326	Irwin et al. (2010)	B4
Tajikistan	GU070327	Irwin et al. (2010)	K2a5
Tajikistan	GU070328	Irwin et al. (2010)	H15a1a1
Tajikistan	GU070329	Irwin et al. (2010)	C4a1a+195
Tajikistan	GU070330	Irwin et al. (2010)	U7a4
Tajikistan	GU070331	Irwin et al. (2010)	D4b2a2a
Tajikistan	GU070332	Irwin et al. (2010)	U4b1a1a1
Tatar	JN857061	Derenko et al. (2012)	N9a2b
Tatar	GU122975	Malyarchuk et al. (2010)	U4a2c
Tatar	GU122976	Malyarchuk et al. (2010)	H10
Tatar	GU122977	Malyarchuk et al. (2010)	H
Tatar	GU122978	Malyarchuk et al. (2010)	K1a
Tatar	GU122979	Malyarchuk et al. (2010)	V
Tatar	GU122980	Malyarchuk et al. (2010)	T1a
Tatar	GU122981	Malyarchuk et al. (2010)	D4e
Tatar	GU122982	Malyarchuk et al. (2010)	U4d
Tatar	GU122983	Malyarchuk et al. (2010)	H1b
Tatar	GU122984	Malyarchuk et al. (2010)	I2
Tatar	GU122985	Malyarchuk et al. (2010)	U4d2
Tatar	GU122986	Malyarchuk et al. (2010)	U3a1
Tatar	GU122987	Malyarchuk et al. (2010)	J1d
Tatar	GU122988	Malyarchuk et al. (2010)	U4d2
Tatar	GU122989	Malyarchuk et al. (2010)	W3
Tatar	GU122990	Malyarchuk et al. (2010)	HV0a
Tatar	GU122991	Malyarchuk et al. (2010)	U5b1
Tatar	GU122992	Malyarchuk et al. (2010)	N1b
Tatar	GU122993	Malyarchuk et al. (2010)	U5a2
Teleut	JN857062	Derenko et al. (2012)	M11c
Teleut	FJ951611	Derenko et al. (2010)	C4d
Teleut	FJ951612	Derenko et al. (2010)	C4a1b2
Teleut	FJ951613	Derenko et al. (2010)	C4a1a1
Teleut	FJ951614	Derenko et al. (2010)	C5c*
Teleut	EF153832	Derenko et al. (2007)	X2e
Teleut	KJ856700	Derenko et al. (2014)	T1*
Teleut	KJ856794	Derenko et al. (2014)	U4b1b1c

Population	GenBank	Reference	Haplogroup (HG)
Tibet	FJ748716	Ji et al. (2012)	D4a5
Tibet	FJ748717	Ji et al. (2012)	M62b2
Tibet	FJ748718	Ji et al. (2012)	A11b
Tibet	FJ748726	Ji et al. (2012)	G3b1
Tibet	FJ748727	Ji et al. (2012)	M30
Tibet	FJ748728	Ji et al. (2012)	B4a1+16311
Tibet	FJ748729	Ji et al. (2012)	M9a1a1c1b1a
Tibet	FJ748730	Ji et al. (2012)	D5a2a1b
Tibet	FJ748731	Ji et al. (2012)	C4a2b2
Tibet	FJ748732	Ji et al. (2012)	A11a
Tibet	FJ748733	Ji et al. (2012)	A11a
Tibet	FJ748734	Ji et al. (2012)	D4l2b
Tibet	FJ748735	Ji et al. (2012)	M9a1b1
Tibet	FJ748736	Ji et al. (2012)	F2h
Tibet	FJ748737	Ji et al. (2012)	F1d
Tibet	FJ748738	Ji et al. (2012)	D4s
Tibet	FJ748739	Ji et al. (2012)	G3b
Tibet	FJ748740	Ji et al. (2012)	G2a1
Tibet	FJ748741	Ji et al. (2012)	M70
Tibet	FJ748742	Ji et al. (2012)	A15a
Tofalar	AY615360.2	Starikovskaya et al. (2005)	C4a1a3a1
Tofalar	AY519492.2	Starikovskaya et al. (2005)	B4a1c2
Tofalar	AY519493.2	Starikovskaya et al. (2005)	Z1
Tofalar	AY195770.2	Mishmar et al. (2003)	B4a1a
Turkey	JQ797783	Pala et al. (2012)	J1b
Turkey	JQ797820	Pala et al. (2012)	J1c2b
Turkey	JQ797969	Pala et al. (2012)	J2b1f
Turkey	JQ797970	Pala et al. (2012)	J2b1f
Turkey	JQ797981	Pala et al. (2012)	T1a1a1
Turkey	JQ797991	Pala et al. (2012)	T1a1a1b
Turkey	JQ797996	Pala et al. (2012)	T1a1a1
Turkey	JQ798018	Pala et al. (2012)	T1a1d
Turkey	JQ798043	Pala et al. (2012)	T1b3
Turkey	HM852846	Schoenberg et al. (2011)	U2d2
Turkey	HM852847	Schoenberg et al. (2011)	U1a1a
Turkey	HM852848	Schoenberg et al. (2011)	A16

Population	GenBank	Reference	Haplogroup (HG)
Turkey	HM852849	Schoenberg et al. (2011)	HV12a
Turkey	HM852850	Schoenberg et al. (2011)	A14
Turkey	HM852851	Schoenberg et al. (2011)	HV4b
Turkey	HM852852	Schoenberg et al. (2011)	U5a1a1
Turkey	HM852853	Schoenberg et al. (2011)	U7a3a
Turkey	HM852854	Schoenberg et al. (2011)	H2a1a
Turkey	HM852855	Schoenberg et al. (2011)	H40
Turkey	HM852856	Schoenberg et al. (2011)	B4b1a3a
Turkmenistan	GU070333	Irwin et al. (2010)	Y1
Turkmenistan	GU070334	Irwin et al. (2010)	K1c
Turkmenistan	GU070335	Irwin et al. (2010)	U7a1a
Turkmenistan	GU070336	Irwin et al. (2010)	H5
Turkmenistan	GU070337	Irwin et al. (2010)	X2d
Turkmenistan	GU070338	Irwin et al. (2010)	H2a2a
Turkmenistan	GU070339	Irwin et al. (2010)	Y1
Turkmenistan	GU070340	Irwin et al. (2010)	M5a2a1a
Turkmenistan	GU070341	Irwin et al. (2010)	C4+152+16093
Turkmenistan	GU070342	Irwin et al. (2010)	F1b1+@152
Turkmenistan	GU070343	Irwin et al. (2010)	J1b3
Turkmenistan	GU070344	Irwin et al. (2010)	M57a
Turkmenistan	GU070345	Irwin et al. (2010)	H1b1g
Turkmenistan	GU070346	Irwin et al. (2010)	C
Turkmenistan	GU070347	Irwin et al. (2010)	T2f1
Turkmenistan	GU070348	Irwin et al. (2010)	F1b1+@152
Turkmenistan	GU070349	Irwin et al. (2010)	H5a4
Turkmenistan	GU070350	Irwin et al. (2010)	U4a1
Turkmenistan	GU070351	Irwin et al. (2010)	C4b3
Turkmenistan	GU070352	Irwin et al. (2010)	M9a1b1
Turkmenistan	GU070353	Irwin et al. (2010)	W4d
Turkmenistan	GU070354	Irwin et al. (2010)	H13c2
Turkmenistan	GU070355	Irwin et al. (2010)	T2b3+151
Turkmenistan	GU070356	Irwin et al. (2010)	X2
Turkmenistan	GU070357	Irwin et al. (2010)	U5b1b1+@16192
Turkmenistan	GU070358	Irwin et al. (2010)	H28
Turkmenistan	GU070359	Irwin et al. (2010)	J1b3
Turkmenistan	GU070360	Irwin et al. (2010)	M57a

Population	GenBank	Reference	Haplogroup (HG)
Turkmenistan	GU070361	Irwin et al. (2010)	G1a1
Turkmenistan	GU070362	Irwin et al. (2010)	J1b3
Turkmenistan	GU070363	Irwin et al. (2010)	M7b1b
Turkmenistan	GU070364	Irwin et al. (2010)	H6a1b1
Turkmenistan	GU070365	Irwin et al. (2010)	J1b
Turkmenistan	GU070366	Irwin et al. (2010)	U4a1
Turkmenistan	GU070367	Irwin et al. (2010)	W
Turkmenistan	GU070368	Irwin et al. (2010)	X2
Turkmenistan	GU070369	Irwin et al. (2010)	M30
Turkmenistan	GU070370	Irwin et al. (2010)	D4g1
Turkmenistan	GU070371	Irwin et al. (2010)	U3
Turkmenistan	GU070372	Irwin et al. (2010)	J1c8a
Turkmenistan	GU070373	Irwin et al. (2010)	M33a1b
Turkmenistan	GU070374	Irwin et al. (2010)	H2a2a
Turkmenistan	GU070375	Irwin et al. (2010)	H2a2a
Turkmenistan	GU070376	Irwin et al. (2010)	F1b1+@152
Turkmenistan	GU070377	Irwin et al. (2010)	C4b3
Turkmenistan	GU070378	Irwin et al. (2010)	H2a2a
Turkmenistan	GU070379	Irwin et al. (2010)	A23
Turkmenistan	GU070380	Irwin et al. (2010)	U5a1g2
Turkmenistan	GU070381	Irwin et al. (2010)	G2a+152
Turkmenistan	GU070382	Irwin et al. (2010)	T
Turkmenistan	GU070383	Irwin et al. (2010)	N
Turkmenistan	GU070384	Irwin et al. (2010)	J1b3
Turkmenistan	GU070385	Irwin et al. (2010)	R11
Turkmenistan	GU070386	Irwin et al. (2010)	U7a3b
Turkmenistan	GU070387	Irwin et al. (2010)	U4a1
Turkmenistan	GU070388	Irwin et al. (2010)	A8a1
Turkmenistan	GU070389	Irwin et al. (2010)	K1a4b
Turkmenistan	GU070390	Irwin et al. (2010)	R0a1a
Turkmenistan	GU070391	Irwin et al. (2010)	U4a1
Turkmenistan	GU070392	Irwin et al. (2010)	D4I2
Turkmenistan	GU070393	Irwin et al. (2010)	K1c
Turkmenistan	GU070394	Irwin et al. (2010)	H2a1
Turkmenistan	GU070395	Irwin et al. (2010)	G1a1
Turkmenistan	GU070396	Irwin et al. (2010)	D4g1

Population	GenBank	Reference	Haplogroup (HG)
Turkmenistan	GU070397	Irwin et al. (2010)	U5a1+@16192
Turkmenistan	GU070398	Irwin et al. (2010)	A8a1
Turkmenistan	GU070399	Irwin et al. (2010)	T
Turkmenistan	GU070400	Irwin et al. (2010)	D4b1a1
Turkmenistan	GU070401	Irwin et al. (2010)	H107
Turkmenistan	GU070402	Irwin et al. (2010)	N
Turkmenistan	GU070403	Irwin et al. (2010)	H2a2a
Turkmenistan	GU070404	Irwin et al. (2010)	A8a1
Turkmenistan	GU070405	Irwin et al. (2010)	H6a1b1
Turkmenistan	GU070406	Irwin et al. (2010)	A23
Turkmenistan	GU070407	Irwin et al. (2010)	M43a1
Turkmenistan	GU070408	Irwin et al. (2010)	H2a1
Turkmenistan	GU070409	Irwin et al. (2010)	H1c
Turkmenistan	GU070410	Irwin et al. (2010)	D4c2a
Turkmenistan	GU070411	Irwin et al. (2010)	H2a2a
Turkmenistan	GU070412	Irwin et al. (2010)	U5a1+@16192
Turkmenistan	GU070413	Irwin et al. (2010)	HV19
Turkmenistan	GU070414	Irwin et al. (2010)	H2a+152 16311
Turkmenistan	GU070415	Irwin et al. (2010)	H5
Turkmenistan	GU070416	Irwin et al. (2010)	HV19
Turkmenistan	GU070417	Irwin et al. (2010)	I
Turkmenistan	GU070418	Irwin et al. (2010)	W+194
Turkmenistan	GU070419	Irwin et al. (2010)	U4a1
Turkmenistan	GU070420	Irwin et al. (2010)	J2b1a
Turkmenistan	GU070421	Irwin et al. (2010)	M57a
Turkmenistan	GU070422	Irwin et al. (2010)	R5a1
Turkmenistan	GU070423	Irwin et al. (2010)	H101
Turkmenistan	GU070424	Irwin et al. (2010)	T
Turkmenistan	GU070425	Irwin et al. (2010)	C
Turkmenistan	GU070426	Irwin et al. (2010)	U2e1
Turkmenistan	GU070427	Irwin et al. (2010)	U2e1
Turkmenistan	GU070428	Irwin et al. (2010)	D4g2a
Turkmenistan	GU070429	Irwin et al. (2010)	T1a1'3
Turkmenistan	GU070430	Irwin et al. (2010)	T1a1'3
Turkmenistan	GU070431	Irwin et al. (2010)	H1c
Turkmenistan	GU070432	Irwin et al. (2010)	J1d

Population	GenBank	Reference	Haplogroup (HG)
Turkmenistan	GU070433	Irwin et al. (2010)	F1b1+@152
Turkmenistan	GU070434	Irwin et al. (2010)	H6a1b1
Turkmenistan	GU070435	Irwin et al. (2010)	C4+152+16093
Turkmenistan	GU070436	Irwin et al. (2010)	G2a1+16189
Turkmenistan	GU070437	Irwin et al. (2010)	I1a1
Turkmenistan	GU070438	Irwin et al. (2010)	K1c
Turkmenistan	GU070439	Irwin et al. (2010)	H1e2c
Turkmenistan	GU070440	Irwin et al. (2010)	D4c2a
Turkmenistan	GU070441	Irwin et al. (2010)	T
Turkmenistan	GU070442	Irwin et al. (2010)	C4+152+16093
Turkmenistan	GU070443	Irwin et al. (2010)	W3a2
Turkmenistan	GU070444	Irwin et al. (2010)	J1b1a1+146
Turkmenistan	GU070445	Irwin et al. (2010)	H107
Turkmenistan	GU070446	Irwin et al. (2010)	H5a4
Turkmenistan	GU070447	Irwin et al. (2010)	M9
Turkmenistan	GU070448	Irwin et al. (2010)	U3
Turkmenistan	GU070449	Irwin et al. (2010)	H1e2c
Turkmenistan	GU070450	Irwin et al. (2010)	R11
Turkmenistan	GU070451	Irwin et al. (2010)	U4a1
Turkmenistan	GU070452	Irwin et al. (2010)	D4I2
Turkmenistan	GU070453	Irwin et al. (2010)	R2
Turkmenistan	GU070454	Irwin et al. (2010)	C4a2a1
Turkmenistan	GU070455	Irwin et al. (2010)	H3ak
Turkmenistan	GU070456	Irwin et al. (2010)	H6a1b1
Turkmenistan	GU070457	Irwin et al. (2010)	R2
Turkmenistan	GU070458	Irwin et al. (2010)	N
Turkmenistan	GU070459	Irwin et al. (2010)	A24
Turkmenistan	GU070460	Irwin et al. (2010)	M57a
Turkmenistan	GU070461	Irwin et al. (2010)	D4I2
Turkmenistan	GU070462	Irwin et al. (2010)	K1c
Turkmenistan	GU070463	Irwin et al. (2010)	X2d
Turkmenistan	GU070464	Irwin et al. (2010)	J1c8a
Turkmenistan	GU070465	Irwin et al. (2010)	F1b1+@152
Turkmenistan	GU070466	Irwin et al. (2010)	X2d
Turkmenistan	GU070467	Irwin et al. (2010)	G1a1
Turkmenistan	GU070468	Irwin et al. (2010)	C4b1

Population	GenBank	Reference	Haplogroup (HG)
Turkmenistan	GU070469	Irwin et al. (2010)	H6a1b1
Turkmenistan	GU070470	Irwin et al. (2010)	G1a1
Turkmenistan	GU070471	Irwin et al. (2010)	F1b1+@152
Turkmenistan	GU070472	Irwin et al. (2010)	I
Turkmenistan	GU070473	Irwin et al. (2010)	M3c+152
Turkmenistan	GU070474	Irwin et al. (2010)	M3a1+204
Turkmenistan	GU070475	Irwin et al. (2010)	H13a1a1d
Turkmenistan	GU070476	Irwin et al. (2010)	F1b1+@152
Turkmenistan	GU070477	Irwin et al. (2010)	D4b1a2a1
Turkmenistan	GU070478	Irwin et al. (2010)	H2a1
Turkmenistan	GU070479	Irwin et al. (2010)	D4b1a2a1
Turkmenistan	GU070480	Irwin et al. (2010)	F2a
Turkmenistan	GU070481	Irwin et al. (2010)	C4+152+16093
Turkmenistan	GU070482	Irwin et al. (2010)	F1b1+@152
Turkmenistan	GU070483	Irwin et al. (2010)	J1b3
Turkmenistan	GU070484	Irwin et al. (2010)	H1c
Turkmenistan	GU070485	Irwin et al. (2010)	M68
Turkmenistan	GU070486	Irwin et al. (2010)	J1b3
Turkmenistan	GU070487	Irwin et al. (2010)	J1b3
Turkmenistan	GU070488	Irwin et al. (2010)	C4b3
Turkmenistan	GU070489	Irwin et al. (2010)	G1a1
Turkmenistan	GU070490	Irwin et al. (2010)	D4b1a1
Turkmenistan	GU070491	Irwin et al. (2010)	U1a
Turkmenistan	GU070492	Irwin et al. (2010)	H6a1b1
Turkmenistan	GU070493	Irwin et al. (2010)	H101
Turkmenistan	GU070494	Irwin et al. (2010)	X2d
Turkmenistan	GU070495	Irwin et al. (2010)	T1a1'3
Turkmenistan	GU070496	Irwin et al. (2010)	N
Turkmenistan	GU070497	Irwin et al. (2010)	C4+152+16093
Turkmenistan	GU070498	Irwin et al. (2010)	D4b1a1
Turkmenistan	GU070499	Irwin et al. (2010)	H1+16189
Turkmenistan	GU070500	Irwin et al. (2010)	F1d
Turkmenistan	GU070501	Irwin et al. (2010)	D4c2a
Turkmenistan	GU070502	Irwin et al. (2010)	R2
Turkmenistan	GU070503	Irwin et al. (2010)	H101
Turkmenistan	GU070504	Irwin et al. (2010)	H13a1a1d

Population	GenBank	Reference	Haplogroup (HG)
Turkmenistan	GU070505	Irwin et al. (2010)	U2a1a
Turkmenistan	GU070506	Irwin et al. (2010)	U1a
Turkmenistan	GU070507	Irwin et al. (2010)	H2a+152 16311
Turkmenistan	GU070508	Irwin et al. (2010)	H1+152
Turkmenistan	GU070509	Irwin et al. (2010)	H1e2c
Turkmenistan	GU070510	Irwin et al. (2010)	T2f1
Turkmenistan	GU070511	Irwin et al. (2010)	B4a1c3a
Turkmenistan	GU070512	Irwin et al. (2010)	U4a1
Turkmenistan	GU070513	Irwin et al. (2010)	C4a2a1
Turkmenistan	GU070514	Irwin et al. (2010)	A11
Turkmenistan	GU070515	Irwin et al. (2010)	U4a1
Turkmenistan	GU070516	Irwin et al. (2010)	M13'46'61+16362
Turkmenistan	GU070517	Irwin et al. (2010)	U4c1
Turkmenistan	GU070518	Irwin et al. (2010)	H2a2a
Turkmenistan	GU070519	Irwin et al. (2010)	T
Turkmenistan	GU070520	Irwin et al. (2010)	D4b1a1
Turkmenistan	GU070521	Irwin et al. (2010)	C4a2a1
Turkmenistan	GU070522	Irwin et al. (2010)	H2a1
Turkmenistan	GU070523	Irwin et al. (2010)	K1c
Turkmenistan	GU070524	Irwin et al. (2010)	H1m1
Turkmenistan	GU070525	Irwin et al. (2010)	F1b1+@152
Turkmenistan	GU070526	Irwin et al. (2010)	J1b
Turkmenistan	GU070527	Irwin et al. (2010)	U2a1a
Turkmenistan	GU070528	Irwin et al. (2010)	C5a2
Turkmenistan	GU070529	Irwin et al. (2010)	N
Turkmenistan	GU070530	Irwin et al. (2010)	H101
Turkmenistan	GU070531	Irwin et al. (2010)	A2r1
Turkmenistan	GU070532	Irwin et al. (2010)	D4g1
Turkmenistan	GU070533	Irwin et al. (2010)	C5a2
Turkmenistan	GU070534	Irwin et al. (2010)	J1b3
Turkmenistan	GU070535	Irwin et al. (2010)	H2a1
Turkmenistan	GU070536	Irwin et al. (2010)	A24
Turkmenistan	GU070537	Irwin et al. (2010)	H2a2a
Turkmenistan	GU070538	Irwin et al. (2010)	H2a1
Turkmenistan	GU070539	Irwin et al. (2010)	U2e2
Turkmenistan	GU070540	Irwin et al. (2010)	D4b1a1

Population	GenBank	Reference	Haplogroup (HG)
Turkmenistan	GU070541	Irwin et al. (2010)	W
Turkmenistan	GU070542	Irwin et al. (2010)	D4j+146
Turkmenistan	GU070543	Irwin et al. (2010)	M37+152+151
Turkmenistan	GU070544	Irwin et al. (2010)	D5a2a1+@16172
Turkmenistan	GU070545	Irwin et al. (2010)	F1b1+@152
Turkmenistan	GU070546	Irwin et al. (2010)	Y1
Turkmenistan	GU070547	Irwin et al. (2010)	G2a1+16189
Turkmenistan	GU070548	Irwin et al. (2010)	J1b3
Turkmenistan	GU070549	Irwin et al. (2010)	J1b1a1+146
Turkmenistan	GU070550	Irwin et al. (2010)	H2a2a
Turkmenistan	GU070551	Irwin et al. (2010)	M5a2a1a
Turkmenistan	GU070552	Irwin et al. (2010)	C4+152+16093
Turkmenistan	GU070553	Irwin et al. (2010)	G2a+152
Turkmenistan	GU070554	Irwin et al. (2010)	H1e2c
Turkmenistan	GU070555	Irwin et al. (2010)	K1a1
Turkmenistan	GU070556	Irwin et al. (2010)	T
Turkmenistan	GU070557	Irwin et al. (2010)	H6a1b1
Turkmenistan	GU070558	Irwin et al. (2010)	J1b3
Turkmenistan	GU070559	Irwin et al. (2010)	D4I2
Turkmenistan	GU070560	Irwin et al. (2010)	H101
Turkmenistan	GU070561	Irwin et al. (2010)	M13'46'61+16362
Turkmenistan	GU070562	Irwin et al. (2010)	H2a2a
Turkmenistan	GU070563	Irwin et al. (2010)	U2e1
Turkmenistan	GU070564	Irwin et al. (2010)	B4b1a3a
Turkmenistan	GU070565	Irwin et al. (2010)	M13'46'61+16362
Turkmenistan	GU070566	Irwin et al. (2010)	H2a2a
Turkmenistan	GU070567	Irwin et al. (2010)	H2a2a
Turkmenistan	GU070568	Irwin et al. (2010)	M13'46'61+16362
Turkmenistan	GU070569	Irwin et al. (2010)	M4b
Turkmenistan	GU070570	Irwin et al. (2010)	N
Turkmenistan	GU070571	Irwin et al. (2010)	T
Turkmenistan	GU070572	Irwin et al. (2010)	D4g1
Turkmenistan	GU070573	Irwin et al. (2010)	R11b1a
Turkmenistan	GU070574	Irwin et al. (2010)	A24
Turkmenistan	GU070575	Irwin et al. (2010)	H2a2a
Turkmenistan	GU070576	Irwin et al. (2010)	I

Population	GenBank	Reference	Haplogroup (HG)
Turkmenistan	GU070577	Irwin et al. (2010)	H1c
Turkmenistan	GU070578	Irwin et al. (2010)	D5a2a1+@16172
Turkmenistan	GU070579	Irwin et al. (2010)	J1b3
Turkmenistan	GU070580	Irwin et al. (2010)	H2a+152 16311
Turkmenistan	GU070581	Irwin et al. (2010)	M30
Tubular	AY519494.2	Starikovskaya et al. (2005)	B4b1a
Tubular	FJ493500	Sukernik et al. (2012)	A1
Tubular	FJ493501	Sukernik et al. (2012)	D3a
Tubular	FJ147306	Sukernik et al. (2012)	X2e
Tubular	FJ147307	Sukernik et al. (2012)	N9a
Tubular	FJ147308	Sukernik et al. (2012)	R9b
Tubular	FJ147309	Sukernik et al. (2012)	HV*
Tubular	FJ147310	Sukernik et al. (2012)	H8
Tubular	FJ147311	Sukernik et al. (2012)	U2e
Tubular	FJ147312	Sukernik et al. (2012)	U4a
Tubular	FJ147313	Sukernik et al. (2012)	U4b
Tubular	FJ147314	Sukernik et al. (2012)	U4b
Tubular	FJ147315	Sukernik et al. (2012)	U4b
Tubular	FJ147316	Sukernik et al. (2012)	U4b
Tubular	FJ147317	Sukernik et al. (2012)	U5a
Tubular	FJ147318	Sukernik et al. (2012)	Z1a
Tubular	FJ147320	Sukernik et al. (2012)	D5c
Tubular	EU482321	Volodko et al. (2008)	C3a
Tubular	EU482335	Volodko et al. (2008)	D5c
Tubular	EU482336	Volodko et al. (2008)	D5c
Tuvinian	JN857063	Derenko et al. (2012)	M9a1a1c1a1
Tuvinian	EU007866	Ingman and Gyllensten (2007)	D4m2
Tuvinian	EU007865	Ingman and Gyllensten (2007)	H35
Tuvinian	EU007864	Ingman and Gyllensten (2007)	G2a1
Tuvinian	EU007863	Ingman and Gyllensten (2007)	D4s
Tuvinian	AY570525.2	Starikovskaya et al. (2005)	D5a2a1
Tuvinian	AY519495.2	Starikovskaya et al. (2005)	B4a1c2
Tuvinian	HM776708	Sukernik et al. (2012)	N9a1
Tuvinian	HM153530	Sukernik et al. (2012)	D3b1
Tuvinian	HM153529	Sukernik et al. (2012)	D3b1
Tuvinian	HM153528	Sukernik et al. (2012)	D6

Population	GenBank	Reference	Haplogroup (HG)
Tuvinian	HM153527	Sukernik et al. (2012)	D6
Tuvinian	FJ858886	Sukernik et al. (2012)	D3a
Tuvinian	FJ493502	Sukernik et al. (2012)	D3b
Tuvinian	EU482385	Volodko et al. (2008)	D3
Tuvinian	KJ856688	Derenko et al. (2014)	H15a1*
Tuvinian	KJ856788	Derenko et al. (2014)	U4d2a
Udegey	AY195772.2	Mishmar et al. (2003)	C4b1
Udegey	FJ493503	Sukernik et al. (2012)	N9b
Udegey	KF148510	Duggan et al. (2013)	M8a1
Udegey	KF148511	Duggan et al. (2013)	C4b1
Udegey	KF148512	Duggan et al. (2013)	M9a1a1a
Udegey	KF148513	Duggan et al. (2013)	Y1a1
Udegey	KF148514	Duggan et al. (2013)	C4b1
Udegey	KF148515	Duggan et al. (2013)	M9a1a1a
Udegey	KF148516	Duggan et al. (2013)	M7a2a3a
Udegey	KF148517	Duggan et al. (2013)	N9b
Udegey	KF148518	Duggan et al. (2013)	M7a2a3a
Udegey	KF148519	Duggan et al. (2013)	M8a1
Udegey	KF148520	Duggan et al. (2013)	M8a1
Udegey	KF148521	Duggan et al. (2013)	M7a2a3a
Udegey	KF148522	Duggan et al. (2013)	C4b1
Udegey	KF148523	Duggan et al. (2013)	C4b1
Udegey	KF148524	Duggan et al. (2013)	M7a2a3a
Udegey	KF148525	Duggan et al. (2013)	Y1a+16189
Udegey	KF148526	Duggan et al. (2013)	C4a1a4a
Udegey	KF148527	Duggan et al. (2013)	C4b1
Ukraine	JQ797787	Pala et al. (2012)	J1c1
Ukraine	JQ797789	Pala et al. (2012)	J1c1b1a
Ukraine	JQ797799	Pala et al. (2012)	J1c2a
Ukraine	JQ797829	Pala et al. (2012)	J1c3f
Ukraine	JQ797831	Pala et al. (2012)	J1c3f
Ukraine	JQ797841	Pala et al. (2012)	J1c4a
Ukraine	JQ797845	Pala et al. (2012)	J1c5a
Ukraine	JQ797859	Pala et al. (2012)	J1c7a1a
Ukraine	JQ798120	Pala et al. (2012)	T2f1
Ukraine	JX266260.1	Mielnik-Sikorska et al. (2013)	C4a1a+195

Population	GenBank	Reference	Haplogroup (HG)
Ukraine	JX266261.1	Mielnik-Sikorska et al. (2013)	C5c1a
Ukraine	JX266262.1	Mielnik-Sikorska et al. (2013)	G2a4
Ukraine	JX307101	Mielnik-Sikorska et al. (2013)	H6a1a
Ukraine	JX128085	Mielnik-Sikorska et al. (2013)	H5a2a
Ukraine	JX128086	Mielnik-Sikorska et al. (2013)	H5b
Ukraine	JX128087	Mielnik-Sikorska et al. (2013)	H5+709
Ukraine	HQ167734	Pala et al. (2012) misc.	T1a
Ukraine	KF146238	Olivieri et al. (2013)	I1a1c
Ukraine	KF146255	Olivieri et al. (2013)	I2
Ukraine	KF146270	Olivieri et al. (2013)	W1
Ulchi	AY615361	Starikovskaya et al. (2005)	C5a1
Ulchi	AY519496.2	Starikovskaya et al. (2005)	C1a
Ulchi	AY519497.2	Starikovskaya et al. (2005)	M8a2b
Ulchi	HM776717	Sukernik et al. (2012)	D4g2b
Ulchi	HM776716	Sukernik et al. (2012)	D4c2
Ulchi	HM776714	Sukernik et al. (2012)	Y1a
Ulchi	HM776713	Sukernik et al. (2012)	Y1a
Ulchi	HM776712	Sukernik et al. (2012)	Y1a
Ulchi	HM776711	Sukernik et al. (2012)	Y1a
Ulchi	HM776710	Sukernik et al. (2012)	Y1a
Ulchi	HM776709	Sukernik et al. (2012)	N9b
Ulchi	HM044856	Sukernik et al. (2012)	D6
Ulchi	HM044855	Sukernik et al. (2012)	D6
Ulchi	HM044854	Sukernik et al. (2012)	Z
Uygur	FJ544242	Zhao et al. (2009)	M62b1a
Uygur	DQ462234	direct submission	C4b
Uzbekistan	GU069236	Irwin et al. (2010)	J1c8a
Uzbekistan	GU069237	Irwin et al. (2010)	H1c
Uzbekistan	GU069238	Irwin et al. (2010)	X2b+226
Uzbekistan	GU069239	Irwin et al. (2010)	X2b+226
Uzbekistan	GU069240	Irwin et al. (2010)	J1b
Uzbekistan	GU069241	Irwin et al. (2010)	U5b1d1a
Uzbekistan	GU069242	Irwin et al. (2010)	M3
Uzbekistan	GU069243	Irwin et al. (2010)	T
Uzbekistan	GU069244	Irwin et al. (2010)	X2b+226
Uzbekistan	GU069245	Irwin et al. (2010)	HV14

Population	GenBank	Reference	Haplogroup (HG)
Uzbekistan	GU069246	Irwin et al. (2010)	T2a1b
Uzbekistan	GU069247	Irwin et al. (2010)	U5a1+@16192
Uzbekistan	GU069248	Irwin et al. (2010)	M4a
Uzbekistan	GU069249	Irwin et al. (2010)	M71
Uzbekistan	GU069250	Irwin et al. (2010)	D4s
Uzbekistan	GU069251	Irwin et al. (2010)	H7a1
Uzbekistan	GU069252	Irwin et al. (2010)	H2a2a
Uzbekistan	GU069253	Irwin et al. (2010)	H13a1a2a
Uzbekistan	GU069254	Irwin et al. (2010)	T2b34
Uzbekistan	GU069255	Irwin et al. (2010)	N1b1
Uzbekistan	GU069256	Irwin et al. (2010)	D4b1b
Uzbekistan	GU069257	Irwin et al. (2010)	H1m1
Uzbekistan	GU069258	Irwin et al. (2010)	D4b2b
Uzbekistan	GU069259	Irwin et al. (2010)	H1e1a6
Uzbekistan	GU069260	Irwin et al. (2010)	C4a2a1
Uzbekistan	GU069261	Irwin et al. (2010)	M7c1
Uzbekistan	GU069262	Irwin et al. (2010)	T1a
Uzbekistan	GU069263	Irwin et al. (2010)	V7b
Uzbekistan	GU069264	Irwin et al. (2010)	D4i
Uzbekistan	GU069265	Irwin et al. (2010)	C4a1
Uzbekistan	GU069266	Irwin et al. (2010)	C5b1
Uzbekistan	GU069267	Irwin et al. (2010)	HV15
Uzbekistan	GU069268	Irwin et al. (2010)	U4c1
Uzbekistan	GU069269	Irwin et al. (2010)	H57
Uzbekistan	GU069270	Irwin et al. (2010)	U5a1a1+152
Uzbekistan	GU069271	Irwin et al. (2010)	U2e1
Uzbekistan	GU069272	Irwin et al. (2010)	A+152+16362
Uzbekistan	GU069273	Irwin et al. (2010)	I1
Uzbekistan	GU069274	Irwin et al. (2010)	M
Uzbekistan	GU069275	Irwin et al. (2010)	T2a+195
Uzbekistan	GU069276	Irwin et al. (2010)	H2a2a
Uzbekistan	GU069277	Irwin et al. (2010)	U7a
Uzbekistan	GU069278	Irwin et al. (2010)	H6
Uzbekistan	GU069279	Irwin et al. (2010)	I1c1
Uzbekistan	GU069280	Irwin et al. (2010)	D4o2a
Uzbekistan	GU069281	Irwin et al. (2010)	C4b8a

Population	GenBank	Reference	Haplogroup (HG)
Uzbekistan	GU069282	Irwin et al. (2010)	H26a1a1
Uzbekistan	GU069283	Irwin et al. (2010)	U4a2b
Uzbekistan	GU069284	Irwin et al. (2010)	W+194
Uzbekistan	GU069285	Irwin et al. (2010)	I4a1
Uzbekistan	GU069286	Irwin et al. (2010)	H5
Uzbekistan	GU069287	Irwin et al. (2010)	K2
Uzbekistan	GU069288	Irwin et al. (2010)	U1b2
Uzbekistan	GU069289	Irwin et al. (2010)	D4o1
Uzbekistan	GU069290	Irwin et al. (2010)	H1e1a4
Uzbekistan	GU069291	Irwin et al. (2010)	U3b2a1a
Uzbekistan	GU069292	Irwin et al. (2010)	G2a+152
Uzbekistan	GU069293	Irwin et al. (2010)	M7c1
Uzbekistan	GU069294	Irwin et al. (2010)	T2
Uzbekistan	GU069295	Irwin et al. (2010)	R2
Uzbekistan	GU069296	Irwin et al. (2010)	H1ag1a
Uzbekistan	GU069297	Irwin et al. (2010)	H28
Uzbekistan	GU069298	Irwin et al. (2010)	D4j+(16286)
Uzbekistan	GU069299	Irwin et al. (2010)	G2b2b
Uzbekistan	GU069300	Irwin et al. (2010)	H5a4
Uzbekistan	GU069301	Irwin et al. (2010)	K1a1
Uzbekistan	GU069302	Irwin et al. (2010)	U4
Uzbekistan	GU069303	Irwin et al. (2010)	T2e
Uzbekistan	GU069304	Irwin et al. (2010)	L1b1a1'4
Uzbekistan	GU069305	Irwin et al. (2010)	T1a+152
Uzbekistan	GU069306	Irwin et al. (2010)	J1c
Uzbekistan	GU069307	Irwin et al. (2010)	T2
Uzbekistan	GU069308	Irwin et al. (2010)	R2
Uzbekistan	GU069309	Irwin et al. (2010)	H1c
Uzbekistan	GU069310	Irwin et al. (2010)	H1b2
Uzbekistan	GU069311	Irwin et al. (2010)	W3a1+199
Uzbekistan	GU069312	Irwin et al. (2010)	A11
Uzbekistan	GU069313	Irwin et al. (2010)	C4a1a+195
Uzbekistan	GU069314	Irwin et al. (2010)	K2a5
Uzbekistan	GU069315	Irwin et al. (2010)	T1a+152
Uzbekistan	GU069316	Irwin et al. (2010)	D4c2a
Uzbekistan	GU069317	Irwin et al. (2010)	H1c

Population	GenBank	Reference	Haplogroup (HG)
Uzbekistan	GU069318	Irwin et al. (2010)	U1a3
Uzbekistan	GU069319	Irwin et al. (2010)	B4m
Uzbekistan	GU069320	Irwin et al. (2010)	N1b1
Uzbekistan	GU069321	Irwin et al. (2010)	H2a+152
Uzbekistan	GU069322	Irwin et al. (2010)	H2a+152 16311
Uzbekistan	GU069323	Irwin et al. (2010)	M7c1
Uzbekistan	GU069324	Irwin et al. (2010)	K3
Uzbekistan	GU069325	Irwin et al. (2010)	C4a1a4a
Uzbekistan	GU069326	Irwin et al. (2010)	C4a1a+195
Uzbekistan	GU069327	Irwin et al. (2010)	I1d
Uzbekistan	GU069328	Irwin et al. (2010)	D5a2a1
Uzbekistan	GU069329	Irwin et al. (2010)	F1b1b
Uzbekistan	GU069330	Irwin et al. (2010)	R1
Uzbekistan	GU069331	Irwin et al. (2010)	T2i
Uzbekistan	GU069332	Irwin et al. (2010)	D5b1b1
Uzbekistan	GU069333	Irwin et al. (2010)	M36
Uzbekistan	GU069334	Irwin et al. (2010)	N
Uzbekistan	GU069181	Irwin et al. (2010)	J1b
Uzbekistan	GU069182	Irwin et al. (2010)	J1b1a1
Uzbekistan	GU069183	Irwin et al. (2010)	C4b1
Uzbekistan	GU069184	Irwin et al. (2010)	B4
Uzbekistan	GU069185	Irwin et al. (2010)	U5b1+16189
Uzbekistan	GU069186	Irwin et al. (2010)	D4a3
Uzbekistan	GU069187	Irwin et al. (2010)	M9
Uzbekistan	GU069188	Irwin et al. (2010)	T2b34
Uzbekistan	GU069189	Irwin et al. (2010)	D4a
Uzbekistan	GU069190	Irwin et al. (2010)	T1a1'3
Uzbekistan	GU069191	Irwin et al. (2010)	H41a
Uzbekistan	GU069192	Irwin et al. (2010)	F1a1a
Uzbekistan	GU069193	Irwin et al. (2010)	D4e5a
Uzbekistan	GU069194	Irwin et al. (2010)	I4a1
Uzbekistan	GU069195	Irwin et al. (2010)	N
Uzbekistan	GU069196	Irwin et al. (2010)	H2a5b1
Uzbekistan	GU069197	Irwin et al. (2010)	M7b1a1a1
Uzbekistan	GU069198	Irwin et al. (2010)	HV6
Uzbekistan	GU069199	Irwin et al. (2010)	M35a

Population	GenBank	Reference	Haplogroup (HG)
Uzbekistan	GU069200	Irwin et al. (2010)	K2a5
Uzbekistan	GU069201	Irwin et al. (2010)	HV2a
Uzbekistan	GU069202	Irwin et al. (2010)	H1a
Uzbekistan	GU069203	Irwin et al. (2010)	C4b1
Uzbekistan	GU069204	Irwin et al. (2010)	T3
Uzbekistan	GU069205	Irwin et al. (2010)	HV1a1
Uzbekistan	GU069206	Irwin et al. (2010)	U5a2e
Uzbekistan	GU069207	Irwin et al. (2010)	D4j+146
Uzbekistan	GU069208	Irwin et al. (2010)	C4a1a3d
Uzbekistan	GU069209	Irwin et al. (2010)	N9a
Uzbekistan	GU069210	Irwin et al. (2010)	A+152+16362
Uzbekistan	GU069211	Irwin et al. (2010)	B4b1b'c
Uzbekistan	GU069212	Irwin et al. (2010)	U5a1a1+152
Uzbekistan	GU069213	Irwin et al. (2010)	F
Uzbekistan	GU069214	Irwin et al. (2010)	H2a+152 16311
Uzbekistan	GU069215	Irwin et al. (2010)	T1a1'3
Uzbekistan	GU069216	Irwin et al. (2010)	I
Uzbekistan	GU069217	Irwin et al. (2010)	U2e1
Uzbekistan	GU069218	Irwin et al. (2010)	U2e1
Uzbekistan	GU069219	Irwin et al. (2010)	U2e1
Uzbekistan	GU069220	Irwin et al. (2010)	U2e1
Uzbekistan	GU069221	Irwin et al. (2010)	U7a3b
Uzbekistan	GU069222	Irwin et al. (2010)	U5b2a1a
Uzbekistan	GU069223	Irwin et al. (2010)	G2a2a
Uzbekistan	GU069224	Irwin et al. (2010)	H101
Uzbekistan	GU069225	Irwin et al. (2010)	U2e1
Uzbekistan	GU069226	Irwin et al. (2010)	D4a
Uzbekistan	GU069227	Irwin et al. (2010)	C4a1a+195
Uzbekistan	GU069228	Irwin et al. (2010)	C4a1a+195
Uzbekistan	GU069229	Irwin et al. (2010)	C4c1b
Uzbekistan	GU069230	Irwin et al. (2010)	D4j
Uzbekistan	GU069231	Irwin et al. (2010)	U3a
Uzbekistan	GU069232	Irwin et al. (2010)	X2e2a2
Uzbekistan	GU069233	Irwin et al. (2010)	M9
Uzbekistan	GU069234	Irwin et al. (2010)	K1c
Uzbekistan	GU069235	Irwin et al. (2010)	J1d2

Population	GenBank	Reference	Haplogroup (HG)
Uzbekistan	GU069106	Irwin et al. (2010)	C4a2a1
Uzbekistan	GU069107	Irwin et al. (2010)	H2a2a
Uzbekistan	GU069108	Irwin et al. (2010)	K1a4b
Uzbekistan	GU069109	Irwin et al. (2010)	H15
Uzbekistan	GU069110	Irwin et al. (2010)	N1b1
Uzbekistan	GU069111	Irwin et al. (2010)	G3a3
Uzbekistan	GU069112	Irwin et al. (2010)	D4q
Uzbekistan	GU069113	Irwin et al. (2010)	H15a1b
Uzbekistan	GU069114	Irwin et al. (2010)	C7+16051
Uzbekistan	GU069115	Irwin et al. (2010)	T
Uzbekistan	GU069116	Irwin et al. (2010)	D4b1a2a1
Uzbekistan	GU069117	Irwin et al. (2010)	HV2
Uzbekistan	GU069118	Irwin et al. (2010)	W
Uzbekistan	GU069119	Irwin et al. (2010)	J1c2
Uzbekistan	GU069120	Irwin et al. (2010)	T2d1
Uzbekistan	GU069121	Irwin et al. (2010)	D4b1a2a1
Uzbekistan	GU069122	Irwin et al. (2010)	R0a+60. 1T
Uzbekistan	GU069123	Irwin et al. (2010)	R0a2c
Uzbekistan	GU069124	Irwin et al. (2010)	T2b34
Uzbekistan	GU069125	Irwin et al. (2010)	M65a+@16311
Uzbekistan	GU069126	Irwin et al. (2010)	A+152+16362
Uzbekistan	GU069127	Irwin et al. (2010)	C4a1a+195
Uzbekistan	GU069128	Irwin et al. (2010)	C4a1a4a
Uzbekistan	GU069129	Irwin et al. (2010)	H20a
Uzbekistan	GU069130	Irwin et al. (2010)	G3a1
Uzbekistan	GU069131	Irwin et al. (2010)	C4a2a1
Uzbekistan	GU069132	Irwin et al. (2010)	I1a1
Uzbekistan	GU069133	Irwin et al. (2010)	U7a
Uzbekistan	GU069134	Irwin et al. (2010)	N
Uzbekistan	GU069135	Irwin et al. (2010)	HV19
Uzbekistan	GU069136	Irwin et al. (2010)	U7a
Uzbekistan	GU069137	Irwin et al. (2010)	T2b34
Uzbekistan	GU069138	Irwin et al. (2010)	D5a2
Uzbekistan	GU069139	Irwin et al. (2010)	D4n2
Uzbekistan	GU069140	Irwin et al. (2010)	U2e1h
Uzbekistan	GU069141	Irwin et al. (2010)	H15

Population	GenBank	Reference	Haplogroup (HG)
Uzbekistan	GU069142	Irwin et al. (2010)	H6
Uzbekistan	GU069143	Irwin et al. (2010)	M7c1
Uzbekistan	GU069144	Irwin et al. (2010)	M61
Uzbekistan	GU069145	Irwin et al. (2010)	D4o1
Uzbekistan	GU069146	Irwin et al. (2010)	W+194
Uzbekistan	GU069147	Irwin et al. (2010)	D5b
Uzbekistan	GU069148	Irwin et al. (2010)	F
Uzbekistan	GU069149	Irwin et al. (2010)	HV0
Uzbekistan	GU069150	Irwin et al. (2010)	H2a2a
Uzbekistan	GU069151	Irwin et al. (2010)	I1a1
Uzbekistan	GU069152	Irwin et al. (2010)	U3
Uzbekistan	GU069153	Irwin et al. (2010)	K1b2
Uzbekistan	GU069154	Irwin et al. (2010)	H15a1b
Uzbekistan	GU069155	Irwin et al. (2010)	H2a2a
Uzbekistan	GU069156	Irwin et al. (2010)	G2a+152
Uzbekistan	GU069157	Irwin et al. (2010)	C4e
Uzbekistan	GU069158	Irwin et al. (2010)	HV14
Uzbekistan	GU069159	Irwin et al. (2010)	U3
Uzbekistan	GU069160	Irwin et al. (2010)	K1a+150
Uzbekistan	GU069161	Irwin et al. (2010)	M65a+@16311
Uzbekistan	GU069162	Irwin et al. (2010)	H2a2a
Uzbekistan	GU069163	Irwin et al. (2010)	U7a4a1
Uzbekistan	GU069164	Irwin et al. (2010)	D4h1
Uzbekistan	GU069165	Irwin et al. (2010)	H1e1a4
Uzbekistan	GU069166	Irwin et al. (2010)	H6
Uzbekistan	GU069167	Irwin et al. (2010)	R2
Uzbekistan	GU069168	Irwin et al. (2010)	M9
Uzbekistan	GU069169	Irwin et al. (2010)	M9
Uzbekistan	GU069170	Irwin et al. (2010)	M43a1
Uzbekistan	GU069171	Irwin et al. (2010)	H5+16311
Uzbekistan	GU069172	Irwin et al. (2010)	J1d2
Uzbekistan	GU069173	Irwin et al. (2010)	H15
Uzbekistan	GU069174	Irwin et al. (2010)	R30b1
Uzbekistan	GU069175	Irwin et al. (2010)	B4a1c3a
Uzbekistan	GU069176	Irwin et al. (2010)	H15
Uzbekistan	GU069177	Irwin et al. (2010)	M38a

Population	GenBank	Reference	Haplogroup (HG)
Uzbekistan	GU069178	Irwin et al. (2010)	F1a2
Uzbekistan	GU069179	Irwin et al. (2010)	H14b1
Uzbekistan	GU069180	Irwin et al. (2010)	K1a+150
Uzbekistan	GU069060	Irwin et al. (2010)	G2b1b
Uzbekistan	GU069061	Irwin et al. (2010)	X2b+226
Uzbekistan	GU069062	Irwin et al. (2010)	X2b+226
Uzbekistan	GU069063	Irwin et al. (2010)	D4m2a
Uzbekistan	GU069064	Irwin et al. (2010)	Z1a
Uzbekistan	GU069065	Irwin et al. (2010)	A8a
Uzbekistan	GU069066	Irwin et al. (2010)	A1a
Uzbekistan	GU069067	Irwin et al. (2010)	R1
Uzbekistan	GU069068	Irwin et al. (2010)	U4
Uzbekistan	GU069069	Irwin et al. (2010)	F1c1a1
Uzbekistan	GU069070	Irwin et al. (2010)	D5a2a1
Uzbekistan	GU069071	Irwin et al. (2010)	H2a+152 16311
Uzbekistan	GU069072	Irwin et al. (2010)	T1a1'3
Uzbekistan	GU069073	Irwin et al. (2010)	D4b2b
Uzbekistan	GU069074	Irwin et al. (2010)	HV6
Uzbekistan	GU069075	Irwin et al. (2010)	U2e1'2'3
Uzbekistan	GU069076	Irwin et al. (2010)	J1c
Uzbekistan	GU069077	Irwin et al. (2010)	U4a1d
Uzbekistan	GU069078	Irwin et al. (2010)	D2b
Uzbekistan	GU069079	Irwin et al. (2010)	H1c
Uzbekistan	GU069080	Irwin et al. (2010)	G2a+152
Uzbekistan	GU069081	Irwin et al. (2010)	G2a+152
Uzbekistan	GU069082	Irwin et al. (2010)	H1c
Uzbekistan	GU069083	Irwin et al. (2010)	B4b1a3a
Uzbekistan	GU069084	Irwin et al. (2010)	C
Uzbekistan	GU069085	Irwin et al. (2010)	A12a
Uzbekistan	GU069086	Irwin et al. (2010)	K1a
Uzbekistan	GU069087	Irwin et al. (2010)	D5a2a1+@16172
Uzbekistan	GU069088	Irwin et al. (2010)	N
Uzbekistan	GU069089	Irwin et al. (2010)	U2e2
Uzbekistan	GU069090	Irwin et al. (2010)	M7b1a2a
Uzbekistan	GU069091	Irwin et al. (2010)	H1e1a3
Uzbekistan	GU069092	Irwin et al. (2010)	T2a+195

Population	GenBank	Reference	Haplogroup (HG)
Uzbekistan	GU069093	Irwin et al. (2010)	H6
Uzbekistan	GU069094	Irwin et al. (2010)	U1a
Uzbekistan	GU069095	Irwin et al. (2010)	D4h1
Uzbekistan	GU069096	Irwin et al. (2010)	C4+152
Uzbekistan	GU069097	Irwin et al. (2010)	Z+152
Uzbekistan	GU069098	Irwin et al. (2010)	H2a2a
Uzbekistan	GU069099	Irwin et al. (2010)	I1
Uzbekistan	GU069100	Irwin et al. (2010)	W6
Uzbekistan	GU069101	Irwin et al. (2010)	L1b1a1'4
Uzbekistan	GU069102	Irwin et al. (2010)	J1c2
Uzbekistan	GU069103	Irwin et al. (2010)	D4j3
Uzbekistan	GU069104	Irwin et al. (2010)	H1e1a3
Uzbekistan	GU069105	Irwin et al. (2010)	U5a1g1
Uzbekistan	GU069007	Irwin et al. (2010)	U5b1b1+@16192
Uzbekistan	GU069008	Irwin et al. (2010)	R5a2b
Uzbekistan	GU069009	Irwin et al. (2010)	Y1
Uzbekistan	GU069010	Irwin et al. (2010)	J1c2i
Uzbekistan	GU069011	Irwin et al. (2010)	C
Uzbekistan	GU069012	Irwin et al. (2010)	R5a2b
Uzbekistan	GU069013	Irwin et al. (2010)	R5a2b
Uzbekistan	GU069014	Irwin et al. (2010)	U5b1b1+@16192
Uzbekistan	GU069015	Irwin et al. (2010)	A8a
Uzbekistan	GU069016	Irwin et al. (2010)	W1+119
Uzbekistan	GU069017	Irwin et al. (2010)	C4a2a1
Uzbekistan	GU069018	Irwin et al. (2010)	A8a
Uzbekistan	GU069019	Irwin et al. (2010)	U5b1b1+@16192
Uzbekistan	GU069020	Irwin et al. (2010)	H1af
Uzbekistan	GU069021	Irwin et al. (2010)	F1b1+@152
Uzbekistan	GU069022	Irwin et al. (2010)	D4e1a1
Uzbekistan	GU069023	Irwin et al. (2010)	D4i
Uzbekistan	GU069024	Irwin et al. (2010)	J1b1b
Uzbekistan	GU069025	Irwin et al. (2010)	D5a2
Uzbekistan	GU069026	Irwin et al. (2010)	H1as1a
Uzbekistan	GU069027	Irwin et al. (2010)	C4a1a4a
Uzbekistan	GU069028	Irwin et al. (2010)	H33c
Uzbekistan	GU069029	Irwin et al. (2010)	H33c

Population	GenBank	Reference	Haplogroup (HG)
Uzbekistan	GU069030	Irwin et al. (2010)	M3d
Uzbekistan	GU069031	Irwin et al. (2010)	U5b1b1+@16192
Uzbekistan	GU069032	Irwin et al. (2010)	C4a1a4a
Uzbekistan	GU069033	Irwin et al. (2010)	A8a
Uzbekistan	GU069034	Irwin et al. (2010)	R0a+60. 1T
Uzbekistan	GU069035	Irwin et al. (2010)	C5a
Uzbekistan	GU069036	Irwin et al. (2010)	F1b1+@152
Uzbekistan	GU069037	Irwin et al. (2010)	G2a+152
Uzbekistan	GU069038	Irwin et al. (2010)	A+152+16362+16189
Uzbekistan	GU069039	Irwin et al. (2010)	HV0+195
Uzbekistan	GU069040	Irwin et al. (2010)	T2d1
Uzbekistan	GU069041	Irwin et al. (2010)	F1a3+16311
Uzbekistan	GU069042	Irwin et al. (2010)	N
Uzbekistan	GU069043	Irwin et al. (2010)	C4a1a4a
Uzbekistan	GU069044	Irwin et al. (2010)	M13'46'61+16362
Uzbekistan	GU069045	Irwin et al. (2010)	M9a'b
Uzbekistan	GU069046	Irwin et al. (2010)	R5a2
Uzbekistan	GU069047	Irwin et al. (2010)	A8a
Uzbekistan	GU069048	Irwin et al. (2010)	HV17
Uzbekistan	GU069049	Irwin et al. (2010)	D4c2a
Uzbekistan	GU069050	Irwin et al. (2010)	M61
Uzbekistan	GU069051	Irwin et al. (2010)	H6b2
Uzbekistan	GU069052	Irwin et al. (2010)	D4g2a
Uzbekistan	GU069053	Irwin et al. (2010)	A8a
Uzbekistan	GU069054	Irwin et al. (2010)	M13'46'61+16362
Uzbekistan	GU069055	Irwin et al. (2010)	U5b1c2
Uzbekistan	GU069056	Irwin et al. (2010)	T2
Uzbekistan	GU069057	Irwin et al. (2010)	N3
Uzbekistan	GU069058	Irwin et al. (2010)	C4b1
Uzbekistan	GU069059	Irwin et al. (2010)	HV0
Yakut	AY882405.1	Achilli et al. (2005)	U5b1b
Yakut	JN857009	Derenko et al. (2012)	B4c1a2
Yakut	FJ951438	Derenko et al. (2010)	C5b1
Yakut	FJ951617	Derenko et al. (2010)	C4b1
Yakut	FJ951618	Derenko et al. (2010)	C4b1
Yakut	EF153831	Derenko et al. (2007)	D2

Population	GenBank	Reference	Haplogroup (HG)
Yakut	EU007862	Ingman and Gyllensten (2007)	T2g1a
Yakut	EU007861	Ingman and Gyllensten (2007)	C4a2a1
Yakut	EU007860	Ingman and Gyllensten (2007)	D5a2a2
Yakut	EU007859	Ingman and Gyllensten (2007)	J15c
Yakut	KJ856681	Derenko et al. (2014)	J2a2b3
Yemen	JQ797915	Pala et al. (2012)	J2a2a1a
Yemen	JQ797916	Pala et al. (2012)	J2a2a1a
Yemen	JQ797933	Pala et al. (2012)	J2a2c1
Yemen	AY882385.2	Achilli et al. (2005)	U3b
Yemen	AY882383	Achilli et al. (2005)	U3a
Yemen	DQ301796	Behar et al. (2006)	K2c
Yemen	DQ301800	Behar et al. (2006)	K1b1b
Yemen	DQ301807	Behar et al. (2006)	K1a7
Yemen	JQ245777	Fernandes et al. (2012)	N1a
Yemen	JQ245778	Fernandes et al. (2012)	W
Yemen	JQ245779	Fernandes et al. (2012)	X2e2
Yemen	JQ245780	Fernandes et al. (2012)	I5a
Yemen	JQ245781	Fernandes et al. (2012)	I5a
Yemen	JQ245782	Fernandes et al. (2012)	I5a
Yemen	JQ245783	Fernandes et al. (2012)	I5a
Yemen	JQ245784	Fernandes et al. (2012)	I5a
Yemen	JQ245785	Fernandes et al. (2012)	I5a
Yemen	JQ245786	Fernandes et al. (2012)	I5a
Yemen	JQ245787	Fernandes et al. (2012)	X2e2
Yukaghir	FJ858885	Sukernik et al. (2012)	D3a1
Yukaghir	FJ858881	Sukernik et al. (2012)	D2b
Yukaghir	FJ858880	Sukernik et al. (2012)	D2b
Yukaghir	FJ493514	Sukernik et al. (2012)	Z1a
Yukaghir	FJ493509	Sukernik et al. (2012)	Z1a
Yukaghir	FJ493510	Sukernik et al. (2012)	Z1a
Yukaghir	FJ493511	Sukernik et al. (2012)	Z1a
Yukaghir	EU482303	Volodko et al. (2008)	C3a
Yukaghir	EU482304	Volodko et al. (2008)	C2a
Yukaghir	EU482305	Volodko et al. (2008)	D3
Yukaghir	EU482306	Volodko et al. (2008)	C3b
Yukaghir	EU482307	Volodko et al. (2008)	C3a

Population	GenBank	Reference	Haplogroup (HG)
Yukaghir	EU482308	Volodko et al. (2008)	D4i
Yukaghir	EU482309	Volodko et al. (2008)	D5a1
Yukaghir	EU482310	Volodko et al. (2008)	C2a
Yukaghir	EU482311	Volodko et al. (2008)	D5a1
Yukaghir	EU482312	Volodko et al. (2008)	C2a
Yukaghir	EU482313	Volodko et al. (2008)	C2a
Yukaghir	EU482314	Volodko et al. (2008)	C2a
Yukaghir	EU482315	Volodko et al. (2008)	C2a

APPENDIX B

TABLES OF GENETIC DISTANCES BASED ON F_{ST} VALUES

Population	Iraq	Kuwait	Iran	Turkey	Cyprus	Israel
Iraq	0	0.00529	0.07835	0.01	0.00975	0.01392
Kuwait	0.00529	0	0.06765	0.01386	0.02566	0.01746
Iran	0.07835	0.06765	0	0.03207	0.13267	0.05083
Turkey	0.01	0.01386	0.03207	0	0.04557	0.00833
Cyprus	0.00975	0.02566	0.13267	0.04557	0	0.01334
Israel	0.01392	0.01746	0.05083	0.00833	0.01334	0
Palestine	0.05041	0.03157	0.16022	0.05977	0.09203	0.08927
Dubai	0.04498	0.02956	0.11528	0.06995	0.06039	0.03048
Yemen	0.09126	0.0816	0.179	0.11665	0.09923	0.07636
Jordan	0.01893	0.02133	0.13716	0.03034	0.03358	0.02875
Lebanon	0.03897	0.04415	0.18355	0.0659	0.04451	0.06741
SaudiArabia	0.0531	0.03007	0.12128	0.04347	0.07584	0.04562
Syria	0.08385	0.06431	0.11129	0.05064	0.11218	0.05984
Albania	0.00616	-0.0048	0.07638	-0.024	0.02897	-0.0096
Romania	0.10553	0.07674	0.09641	0.07329	0.16075	0.11109
Bosnia	-0.0411	-0.0358	0.07633	-0.0496	-0.0405	-0.0454
Belarus	0.08748	0.08389	0.20195	0.08967	0.10501	0.11159
Lithuania	0.03169	0.02136	0.05811	0.02142	0.06258	0.02323
Russia	0.01583	0.0312	0.17143	0.06211	0.02163	0.07069
Ukraine	0.05297	0.03625	0.08091	0.03879	0.08821	0.04363
Poland	0.05678	0.05105	0.18908	0.07792	0.08152	0.09153
Bulgaria	-0.0007	0.01113	0.08711	0.02239	0.01245	0.01107
Chuvash	0.18866	0.16525	0.28048	0.19221	0.22141	0.17232
CzechRepublic	0.02107	0.02964	0.18035	0.05591	0.03399	0.07186
Estonia	0.02949	0.02162	-0.0344	-0.0228	0.07845	-0.024
Hungary	0.00402	0.01843	0.11853	0.03576	0.01613	0.04173
Kalmyk	0.04678	0.02404	0.16369	0.04673	0.07353	0.04042
Moldova	-0.0488	-0.0361	0.09636	-0.0294	-0.0254	-0.0096
Slovakia	0.05231	0.05632	0.21413	0.09291	0.07219	0.1118
Tatar	0.00176	0.0082	0.1145	0.01906	0.01442	0.02317
Csango	0.01706	0.0218	0.12157	0.04221	0.01432	0.01419

Population	Iraq	Kuwait	Iran	Turkey	Cyprus	Israel
Roma	0.07001	0.06119	0.17708	0.11976	0.08609	0.091
Szekely	0.00657	0.01693	0.11589	0.03235	0.01745	0.03392
NorthOssetian	0.03018	0.00961	0.06413	0.02352	0.05986	0.00293
Adygei	-0.0092	-0.0022	0.15535	0.0077	0.00043	0.00156
Dargin	-0.0556	-0.0375	0.1407	-0.0002	-0.0277	0.02207
Armenia	-0.0097	-0.005	0.09632	0.00834	0.00018	0.00477
Azerbaijan	0.01314	0.01712	0.03416	-0.0141	0.0451	0.01151
Georgia	0.00465	0.01913	0.1147	0.01423	0.00945	0.02435
Kazakhstan	0.03818	0.03033	0.14864	0.05416	0.05195	0.05919
Uzbekistan	0.01923	0.01797	0.1241	0.04191	0.02992	0.03816
Kyrgyzstan	0.0518	0.04001	0.16201	0.07579	0.06734	0.07196
Tajikistan	0.03087	0.02667	0.1197	0.04832	0.04294	0.04031
Turkmenistan	0.01803	0.01529	0.13189	0.04054	0.03356	0.04724
Pakistan	0.02702	0.02244	0.17084	0.03188	0.04978	0.05043
Tibet	0.17264	0.14343	0.28617	0.17438	0.20181	0.18261
Afghanistan	0.03074	0.04243	0.15593	0.06285	0.01843	0.03577
India	0.21427	0.16873	0.40418	0.27647	0.26416	0.29411
Nepal	0.08944	0.07058	0.19629	0.12702	0.1114	0.09737
AltaianKazakh	0.01167	0.01895	0.18445	0.04221	0.01942	0.05995
AltaianKizhi	0.11832	0.09612	0.22764	0.14979	0.1373	0.12451
Buryat	0.08272	0.06338	0.20355	0.11162	0.10793	0.1042
Ket	0.08108	0.04956	0.21841	0.08081	0.10808	0.07489
Khamnigan	0.10134	0.07784	0.21885	0.12538	0.1252	0.11403
Shor	0.06791	0.05265	0.19031	0.09767	0.08941	0.08517
Teleut	0.086	0.06928	0.16964	0.10072	0.11057	0.07376
Tofalar	0.08738	0.05908	0.18509	0.09778	0.12244	0.08874
Tubular	0.06706	0.06218	0.16044	0.07026	0.08393	0.06652
Tuvinian	0.09714	0.0712	0.24333	0.12063	0.12384	0.12589
Uyghur	0.10405	0.05781	0.2216	0.10141	0.14333	0.05936
Evenki	0.16752	0.13559	0.29183	0.20058	0.19864	0.19309
Mansi	0.04659	0.03013	0.14814	0.04728	0.07644	0.06106
Nganasan	0.12468	0.1003	0.24921	0.15745	0.14804	0.14082
Yakut	0.06465	0.04396	0.14989	0.07254	0.09664	0.06525
Chukchi	0.2587	0.22411	0.41537	0.30436	0.2871	0.30618
Even	0.13797	0.10788	0.27026	0.17137	0.17287	0.17202
Koryak	0.13586	0.11114	0.23574	0.17316	0.1618	0.15388

Population	Iraq	Kuwait	Iran	Turkey	Cyprus	Israel
Negidal	0.08133	0.05234	0.18061	0.08174	0.11378	0.07844
Nivkhi	0.15658	0.1352	0.24127	0.18503	0.19857	0.1977
Udegey	0.15716	0.13228	0.29588	0.20858	0.18732	0.19997
Ulchi	0.07748	0.05726	0.16891	0.10117	0.10732	0.08902
Yukaghir	0.17783	0.14605	0.30668	0.21963	0.21096	0.21228
Bargut	0.09579	0.06686	0.23674	0.12851	0.12591	0.12536
Han	0.12199	0.10282	0.23966	0.12283	0.14142	0.12689
Mongolia	0.03292	0.02078	0.11572	0.0492	0.04747	0.00988
China	0.07186	0.06074	0.17429	0.09393	0.0851	0.08901

Population	Palestine	Dubai	Yemen	Jordan	Lebanon	SaudiArabia
Iraq	0.05041	0.04498	0.0913	0.0189	0.03897	0.0531
Kuwait	0.03157	0.02956	0.0816	0.0213	0.04415	0.03007
Iran	0.16022	0.11528	0.179	0.1372	0.18355	0.12128
Turkey	0.05977	0.06995	0.1167	0.0303	0.0659	0.04347
Cyprus	0.09203	0.06039	0.0992	0.0336	0.04451	0.07584
Israel	0.08927	0.03048	0.0764	0.0288	0.06741	0.04562
Palestine	0	0.12396	0.1901	0.1149	0.09537	0.03746
Dubai	0.12396	0	0.0105	0.0663	0.12231	0.04829
Yemen	0.1901	0.01045	0	0.1177	0.14521	0.10827
Jordan	0.11494	0.0663	0.1177	0	0.09752	0.05874
Lebanon	0.09537	0.12231	0.1452	0.0975	0	0.09786
SaudiArabia	0.03746	0.04829	0.1083	0.0587	0.09786	0
Syria	0.11136	0.16239	0.1736	0.1503	0.13649	0.09108
Albania	0.04523	0.0644	0.0758	0.0354	0.05262	0.02407
Romania	0.1065	0.16308	0.2032	0.1904	0.18017	0.11613
Bosnia	0.02037	0.02755	0.0754	0.0068	-0.0016	-0.01065
Belarus	0.16587	0.1622	0.1995	0.1427	0.11328	0.15135
Lithuania	0.07775	0.02027	0.0482	0.0618	0.10116	0.05387
Russia	0.09683	0.10813	0.155	0.0716	0.07497	0.09922
Ukraine	0.09083	0.07085	0.1139	0.097	0.11449	0.07219
Poland	0.06457	0.10497	0.1668	0.061	0.1082	0.08292
Bulgaria	0.09683	0.0388	0.0942	0.0429	0.07986	0.04693
Chuvash	0.24026	0.12604	0.1505	0.2128	0.28013	0.16272
CzechRepublic	0.07815	0.09938	0.1548	0.0527	0.07479	0.07097

Population	Palestine	Dubai	Yemen	Jordan	Lebanon	SaudiArabia
Estonia	0.10624	0.0471	0.1155	0.0916	0.12237	0.06314
Hungary	0.08396	0.0803	0.1311	0.0545	0.06359	0.08746
Kalmyk	0.1398	0.04951	0.0852	0.0326	0.12273	0.03089
Moldova	0.00765	0.03057	0.0666	0.0156	0.0159	0.0153
Slovakia	0.12156	0.14292	0.1926	0.0981	0.11634	0.1092
Tatar	0.09684	0.03639	0.0858	0.0443	0.05192	0.04567
Csango	0.09771	0.06668	0.1012	0.0505	0.06521	0.07807
Roma	0.17262	0.05804	0.1052	0.0942	0.1483	0.09916
Szekely	0.06862	0.06374	0.1173	0.044	0.05803	0.06725
NorthOssetian	0.09271	-0.018	0.029	0.036	0.09185	0.03549
Adygei	0.06527	0.02307	0.0605	0.0209	-0.0204	0.02768
Dargin	0.04343	0.03857	0.108	0.0464	0.09654	0.00274
Armenia	0.05462	0.02922	0.0847	0.0252	0.03025	0.01494
Azerbaijan	0.08037	0.06961	0.1263	0.0503	0.06706	0.04585
Georgia	0.09623	0.08426	0.1146	0.0417	0.05186	0.04558
Kazakhstan	0.08528	0.06496	0.1078	0.0403	0.06969	0.05617
Uzbekistan	0.0795	0.04856	0.087	0.0271	0.05647	0.04859
Kyrgyzstan	0.11423	0.06817	0.1034	0.0565	0.08597	0.06333
Tajikistan	0.10309	0.04393	0.0913	0.0192	0.0673	0.05562
Turkmenistan	0.08465	0.05592	0.1089	0.0321	0.06964	0.05286
Pakistan	0.10551	0.09117	0.1442	0.0346	0.09419	0.07539
Tibet	0.23552	0.17016	0.2027	0.1779	0.22982	0.07811
Afghanistan	0.12959	0.07927	0.0956	0.0345	0.06601	0.09169
India	0.33838	0.29254	0.2944	0.3251	0.32613	0.21443
Nepal	0.22732	0.07557	0.1201	0.1002	0.1918	0.08135
AltaianKazakh	0.06861	0.08404	0.135	0.0397	0.06713	0.03784
AltaianKizhi	0.2004	0.09284	0.1278	0.1317	0.17944	0.09788
Buryat	0.16926	0.07375	0.1191	0.0925	0.14613	0.08684
Ket	0.16976	0.05861	0.0946	0.0843	0.18934	0.03451
Khamnigan	0.17364	0.08669	0.1251	0.1133	0.15842	0.08359
Shor	0.13191	0.08742	0.1211	0.0934	0.13247	0.05689
Teleut	0.1916	0.0516	0.1038	0.099	0.18145	0.0711
Tofalar	0.16138	0.06184	0.1285	0.0981	0.1867	0.05665
Tubular	0.11905	0.0808	0.1132	0.0462	0.1068	0.04217
Tuvinian	0.14913	0.11898	0.1601	0.1187	0.15222	0.05952
Uyghur	0.22374	0.03092	0.077	0.118	0.20341	0.05367

Population	Palestine	Dubai	Yemen	Jordan	Lebanon	SaudiArabia
Evenki	0.24749	0.17244	0.2006	0.1967	0.23825	0.13355
Mansi	0.11235	0.07037	0.1172	0.0756	0.11289	0.01436
Nganasan	0.23727	0.11677	0.1552	0.1657	0.20912	0.09049
Yakut	0.1216	0.08397	0.1152	0.1034	0.10926	0.06476
Chukchi	0.34175	0.29755	0.3194	0.3468	0.33718	0.26274
Even	0.25449	0.1598	0.1878	0.1949	0.24738	0.0868
Koryak	0.25723	0.11588	0.1698	0.1706	0.23708	0.13118
Negidal	0.10562	0.05621	0.1144	0.0791	0.14555	0.01387
Nivkhi	0.23911	0.23985	0.279	0.26	0.28817	0.14352
Udegey	0.29545	0.19085	0.2074	0.2364	0.26659	0.13396
Ulchi	0.15115	0.07998	0.1303	0.1087	0.17157	0.06081
Yukaghir	0.29782	0.1921	0.2152	0.2164	0.271	0.1665
Bargut	0.15565	0.1161	0.149	0.11	0.14639	0.0857
Han	0.19426	0.11784	0.1413	0.1254	0.1724	0.05394
Mongolia	0.13114	0.0161	0.0449	0.0452	0.10793	0.03215
China	0.12568	0.08001	0.0996	0.0528	0.08804	0.08146

Population	Syria	Albania	Romania	Bosnia	Belarus	Lithuania
Iraq	0.08385	0.00616	0.10553	-0.0411	0.08748	0.03169
Kuwait	0.06431	-0.0048	0.07674	-0.0358	0.08389	0.02136
Iran	0.11129	0.07638	0.09641	0.07633	0.20195	0.05811
Turkey	0.05064	-0.024	0.07329	-0.0496	0.08967	0.02142
Cyprus	0.11218	0.02897	0.16075	-0.0405	0.10501	0.06258
Israel	0.05984	-0.0096	0.11109	-0.0454	0.11159	0.02323
Palestine	0.11136	0.04523	0.1065	0.02037	0.16587	0.07775
Dubai	0.16239	0.0644	0.16308	0.02755	0.1622	0.02027
Yemen	0.17358	0.07579	0.20317	0.07538	0.19954	0.04815
Jordan	0.1503	0.03543	0.19035	0.00677	0.14267	0.06182
Lebanon	0.13649	0.05262	0.18017	-0.0016	0.11328	0.10116
SaudiArabia	0.09108	0.02407	0.11613	-0.0107	0.15135	0.05387
Syria	0	-0.0737	0.06214	0.00733	0.20769	0.06224
Albania	-0.0737	0	0.00039	-0.1117	0.09991	-0.0282
Romania	0.06214	0.00039	0	0.05602	0.19287	0.04055
Bosnia	0.00733	-0.1117	0.05602	0	-0.0049	-0.0306
Belarus	0.20769	0.09991	0.19287	-0.0049	0	0.10943

Population	Syria	Albania	Romania	Bosnia	Belarus	Lithuania
Lithuania	0.06224	-0.0282	0.04055	-0.0306	0.10943	0
Russia	0.18057	0.07505	0.17951	-0.0168	0.11486	0.08749
Ukraine	0.07555	-0.0266	0.0259	-0.0242	0.11596	-0.0034
Poland	0.16872	0.06082	0.1655	0.00728	0.13721	0.09689
Bulgaria	0.17637	0.06567	0.15598	-0.0049	0.13339	0.03939
Chuvash	0.28834	0.12019	0.31217	0.15399	0.3086	0.15264
CzechRepublic	0.17774	0.07697	0.18322	-0.015	0.12608	0.09355
Estonia	0.0852	-0.0164	0.03759	-0.0201	0.11769	-0.0187
Hungary	0.14109	0.04749	0.14554	-0.0262	0.10739	0.0583
Kalmyk	0.12912	0.01674	0.15086	0.03492	0.15976	0.04083
Moldova	0.02432	-0.0953	0.06167	-0.1014	0.08981	-0.0194
Slovakia	0.21362	0.11242	0.21341	0.01485	0.15506	0.13568
Tatar	0.13773	0.03445	0.14978	-0.0386	0.085	0.03858
Csango	0.10211	0.0209	0.12873	-0.0322	0.10224	0.05285
Roma	0.22602	0.10685	0.20744	0.07826	0.18901	0.09292
Szekely	0.13477	0.03386	0.12977	-0.0323	0.09454	0.0493
NorthOssetian	0.0644	-0.01	0.09494	-0.0136	0.12008	-0.0108
Adygei	0.15275	-0.0019	0.17357	-0.0816	-0.0191	0.01129
Dargin	0.18134	0.00527	0.12444	0.01457	0.1699	0.00975
Armenia	0.09259	-0.0091	0.10593	-0.0825	0.09151	0.01144
Azerbaijan	0.10511	0.01959	0.10595	-0.0267	0.10751	0.03413
Georgia	0.10906	0.03089	0.1539	-0.0624	0.10982	0.0622
Kazakhstan	0.12826	0.04	0.14154	0.0043	0.11073	0.07142
Uzbekistan	0.12036	0.02549	0.13233	-0.013	0.10472	0.04872
Kyrgyzstan	0.15508	0.0532	0.1597	0.02308	0.1272	0.07506
Tajikistan	0.14347	0.04721	0.15985	0.00012	0.10302	0.05812
Turkmenistan	0.13172	0.03886	0.13507	-0.0109	0.11654	0.05596
Pakistan	0.1453	0.00917	0.17831	-0.0048	0.13093	0.08575
Tibet	0.24495	0.1521	0.26208	0.13185	0.2693	0.18851
Afghanistan	0.11321	0.04032	0.18856	-0.0078	0.14021	0.07813
India	0.4326	0.31654	0.33894	0.36453	0.36112	0.29145
Nepal	0.24122	0.13177	0.21841	0.11497	0.23347	0.1108
AltaianKazakh	0.15801	0.05541	0.17241	-0.0175	0.12868	0.07382
AltaianKizhi	0.22596	0.10683	0.22515	0.10718	0.21896	0.1249
Buryat	0.22861	0.08519	0.2097	0.07886	0.18265	0.10611
Ket	0.15163	0.01344	0.1749	0.06696	0.23095	0.07216

Population	Syria	Albania	Romania	Bosnia	Belarus	Lithuania
Khamnigan	0.22741	0.09848	0.20595	0.09554	0.1987	0.11622
Shor	0.17605	0.05825	0.18206	0.0497	0.18653	0.08834
Teleut	0.20019	0.07115	0.20135	0.08075	0.21532	0.08645
Tofalar	0.18673	0.01012	0.19826	0.01732	0.20551	0.07228
Tubular	0.12805	0.03322	0.17655	-0.0178	0.1271	0.07506
Tuvinian	0.22223	0.11048	0.20404	0.09646	0.20373	0.12152
Uyghur	0.16748	-0.0219	0.20773	0.08846	0.2577	0.04687
Evenki	0.28275	0.16067	0.26606	0.18363	0.27865	0.18583
Mansi	0.11687	0.02311	0.13068	-0.0099	0.13906	0.0556
Nganasan	0.25312	0.1337	0.23248	0.13144	0.24564	0.14131
Yakut	0.13465	0.0031	0.12295	0.02734	0.14063	0.04623
Chukchi	0.42172	0.32523	0.35852	0.32792	0.37902	0.31111
Even	0.29176	0.15778	0.23639	0.1817	0.28074	0.16212
Koryak	0.28495	0.15835	0.25024	0.15199	0.25297	0.1551
Negidal	0.16209	0.04176	0.16207	0.0387	0.18716	0.05267
Nivkhi	0.3432	0.24073	0.28441	0.20744	0.318	0.22067
Udegey	0.32652	0.1793	0.27965	0.19547	0.30208	0.21208
Ulchi	0.20422	0.08244	0.18221	0.07902	0.20591	0.09046
Yukaghir	0.30901	0.18529	0.28931	0.22394	0.30536	0.20484
Bargut	0.2163	0.09055	0.20348	0.09652	0.19099	0.12093
Han	0.18959	0.07735	0.2232	0.05503	0.21575	0.13258
Mongolia	0.1042	0.02213	0.14667	0.01759	0.16655	0.03427
China	0.1496	0.04884	0.18084	0.03676	0.13565	0.08853

Population	Russia	Ukraine	Poland	Bulgaria	Chuvash	CzechR
Iraq	0.01583	0.05297	0.05678	-0.0007	0.1887	0.02107
Kuwait	0.0312	0.03625	0.05105	0.01113	0.1653	0.02964
Iran	0.17143	0.08091	0.18908	0.08711	0.2805	0.18035
Turkey	0.06211	0.03879	0.07792	0.02239	0.1922	0.05591
Cyprus	0.02163	0.08821	0.08152	0.01245	0.2214	0.03399
Israel	0.07069	0.04363	0.09153	0.01107	0.1723	0.07186
Palestine	0.09683	0.09083	0.06457	0.09683	0.2403	0.07815
Dubai	0.10813	0.07085	0.10497	0.0388	0.126	0.09938
Yemen	0.15499	0.11385	0.16676	0.09422	0.1505	0.1548
Jordan	0.07155	0.097	0.06096	0.04286	0.2128	0.0527

Population	Russia	Ukraine	Poland	Bulgaria	Chuvash	CzechR
Lebanon	0.07497	0.11449	0.1082	0.07986	0.2801	0.07479
SaudiArabia	0.09922	0.07219	0.08292	0.04693	0.1627	0.07097
Syria	0.18057	0.07555	0.16872	0.17637	0.2883	0.17774
Albania	0.07505	-0.0266	0.06082	0.06567	0.1202	0.07697
Romania	0.17951	0.0259	0.1655	0.15598	0.3122	0.18322
Bosnia	-0.0168	-0.0242	0.00728	-0.0049	0.154	-0.015
Belarus	0.11486	0.11596	0.13721	0.13339	0.3086	0.12608
Lithuania	0.08749	-0.0034	0.09689	0.03939	0.1526	0.09355
Russia	0	0.10161	0.06962	0.01746	0.2918	0.01911
Ukraine	0.10161	0	0.07729	0.08175	0.2291	0.09887
Poland	0.06962	0.07729	0	0.08653	0.2556	0.0074
Bulgaria	0.01746	0.08175	0.08653	0	0.2246	0.03654
Chuvash	0.2918	0.22909	0.25564	0.22457	0	0.2572
CzechRepublic	0.01911	0.09887	0.0074	0.03654	0.2572	0
Estonia	0.11033	-0.0143	0.10198	0.03864	0.2087	0.11774
Hungary	0.00387	0.07706	0.07202	0.00487	0.2696	0.02591
Kalmyk	0.13078	0.06688	0.09283	0.09475	0.2155	0.08275
Moldova	-0.0242	-0.0106	-0.0295	0.00836	0.1656	-0.0193
Slovakia	0.05819	0.12592	0.01279	0.07681	0.2913	-0.0241
Tatar	0.01632	0.07222	0.07356	-0.0106	0.2123	0.0127
Csango	0.03901	0.06341	0.08599	0.03158	0.2243	0.04967
Roma	0.09648	0.10144	0.12968	0.06664	0.26	0.11769
Szekely	0.00418	0.06034	0.05682	0.00165	0.2271	0.02126
NorthOssetian	0.09934	0.01421	0.07507	0.03991	0.1479	0.08173
Adygei	0.03214	0.06762	0.05633	0.02447	0.1074	0.02744
Dargin	-0.0567	0.06948	0.01245	-0.0129	0.2232	-0.03
Armenia	0.01455	0.0325	0.06197	-0.0023	0.188	0.02262
Azerbaijan	0.06408	0.05671	0.09543	0.00982	0.2184	0.06717
Georgia	0.03001	0.09345	0.09488	0.0124	0.2134	0.02274
Kazakhstan	0.06139	0.07183	0.06043	0.05422	0.2266	0.04708
Uzbekistan	0.0391	0.06136	0.05961	0.02436	0.2088	0.03635
Kyrgyzstan	0.08171	0.07702	0.08516	0.06443	0.215	0.0716
Tajikistan	0.05658	0.07693	0.07379	0.02763	0.1765	0.05307
Turkmenistan	0.03861	0.06183	0.06441	0.03149	0.2344	0.03879
Pakistan	0.0957	0.10914	0.08517	0.07257	0.1831	0.0557
Tibet	0.24908	0.18487	0.18129	0.2197	0.3239	0.20258

Population	Russia	Ukraine	Poland	Bulgaria	Chuvash	CzechR
Afghanistan	0.05865	0.1156	0.11312	0.04137	0.2292	0.0635
India	0.30678	0.24812	0.24921	0.35545	0.5151	0.31233
Nepal	0.16084	0.10907	0.14821	0.12324	0.2709	0.15875
AltaianKazakh	0.00979	0.09444	0.04451	0.02554	0.2473	-0.0126
AltaianKizhi	0.18567	0.11719	0.15682	0.14256	0.1897	0.1689
Buryat	0.14425	0.09973	0.13013	0.11323	0.1633	0.13399
Ket	0.19049	0.10286	0.10749	0.15647	0.2063	0.14984
Khamnigan	0.16453	0.10885	0.13703	0.13093	0.1545	0.14358
Shor	0.12236	0.09308	0.10186	0.09165	0.1626	0.08508
Teleut	0.16664	0.09606	0.15139	0.10232	0.1892	0.15409
Tofalar	0.18268	0.0957	0.13097	0.13321	0.0464	0.15795
Tubular	0.11642	0.10993	0.10652	0.06656	0.1347	0.06472
Tuvinian	0.16155	0.11596	0.11246	0.15063	0.2974	0.1279
Uyghur	0.23867	0.06426	0.12827	0.19266	0.1895	0.19237
Evenki	0.2446	0.16087	0.18923	0.22418	0.3212	0.22703
Mansi	0.10576	0.07047	0.09006	0.07793	0.2071	0.06134
Nganasan	0.19705	0.12528	0.16817	0.16496	0.3146	0.17602
Yakut	0.13273	0.02764	0.10151	0.10418	0.2075	0.13007
Chukchi	0.34629	0.29244	0.27813	0.35408	0.4496	0.32245
Even	0.21901	0.14275	0.18226	0.21278	0.3727	0.21565
Koryak	0.21029	0.14062	0.20413	0.18175	0.2826	0.22667
Negidal	0.15581	0.06693	0.08874	0.11051	0.1983	0.10914
Nivkhi	0.24489	0.22425	0.27084	0.22164	0.3411	0.27738
Udegey	0.23377	0.17609	0.21886	0.22353	0.338	0.24653
Ulchi	0.15119	0.10092	0.14885	0.11238	0.2	0.15754
Yukaghir	0.26192	0.17987	0.22268	0.25115	0.3698	0.26258
Bargut	0.16468	0.10597	0.10738	0.15298	0.2877	0.13235
Han	0.18832	0.13926	0.14855	0.16409	0.2456	0.1567
Mongolia	0.10823	0.06852	0.11014	0.05212	0.1662	0.08547
China	0.10215	0.09467	0.09097	0.08731	0.1774	0.08893

Population	Estonia	Hungary	Kalmyk	Moldova	Slovakia	Tatar
Iraq	0.02949	0.00402	0.04678	-0.0488	0.05231	0.00176
Kuwait	0.02162	0.01843	0.02404	-0.0361	0.05632	0.0082
Iran	-0.0344	0.11853	0.16369	0.09636	0.21413	0.1145

Population	Estonia	Hungary	Kalmyk	Moldova	Slovakia	Tatar
Turkey	-0.0228	0.03576	0.04673	-0.0294	0.09291	0.01906
Cyprus	0.07845	0.01613	0.07353	-0.0254	0.07219	0.01442
Israel	-0.024	0.04173	0.04042	-0.0096	0.1118	0.02317
Palestine	0.10624	0.08396	0.1398	0.00765	0.12156	0.09684
Dubai	0.0471	0.0803	0.04951	0.03057	0.14292	0.03639
Yemen	0.11554	0.13111	0.08521	0.06664	0.1926	0.0858
Jordan	0.09155	0.05447	0.03261	0.01558	0.09813	0.04426
Lebanon	0.12237	0.06359	0.12273	0.0159	0.11634	0.05192
SaudiArabia	0.06314	0.08746	0.03089	0.0153	0.1092	0.04567
Syria	0.0852	0.14109	0.12912	0.02432	0.21362	0.13773
Albania	-0.0164	0.04749	0.01674	-0.0953	0.11242	0.03445
Romania	0.03759	0.14554	0.15086	0.06167	0.21341	0.14978
Bosnia	-0.0201	-0.0262	0.03492	-0.1014	0.01485	-0.0386
Belarus	0.11769	0.10739	0.15976	0.08981	0.15506	0.085
Lithuania	-0.0187	0.0583	0.04083	-0.0194	0.13568	0.03858
Russia	0.11033	0.00387	0.13078	-0.0242	0.05819	0.01632
Ukraine	-0.0143	0.07706	0.06688	-0.0106	0.12592	0.07222
Poland	0.10198	0.07202	0.09283	-0.0295	0.01279	0.07356
Bulgaria	0.03864	0.00487	0.09475	0.00836	0.07681	-0.0106
Chuvash	0.20868	0.26957	0.21546	0.16555	0.2913	0.21227
CzechRepublic	0.11774	0.02591	0.08275	-0.0193	-0.0241	0.0127
Estonia	0	0.06121	0.08772	0.02031	0.15603	0.05256
Hungary	0.06121	0	0.10105	-0.0372	0.06306	0.00658
Kalmyk	0.08772	0.10105	0	0.07214	0.13747	0.03879
Moldova	0.02031	-0.0372	0.07214	0	0.01497	-0.0023
Slovakia	0.15603	0.06306	0.13747	0.01497	0	0.05214
Tatar	0.05256	0.00658	0.03879	-0.0023	0.05214	0
Csango	0.05566	0.02718	0.07912	-0.0066	0.08044	0.02564
Roma	0.12224	0.08034	0.07395	0.05227	0.15641	0.06616
Szekely	0.05	0.00109	0.07584	-0.0351	0.05719	0.00281
NorthOssetian	-0.0054	0.06764	-0.0008	-0.0148	0.11636	0.02348
Adygei	0.05087	0.02601	0.04631	-0.0092	0.0783	-0.0192
Dargin	0.10264	-0.0425	0.09663	-0.0223	0.03786	-0.0207
Armenia	0.03465	0.00439	0.04484	-0.0512	0.06561	-0.013
Azerbaijan	-0.0125	0.03692	0.09663	0.00754	0.10249	0.02541
Georgia	0.07454	0.01935	0.08316	-0.0059	0.06534	-0.0051

Population	Estonia	Hungary	Kalmyk	Moldova	Slovakia	Tatar
Kazakhstan	0.08574	0.05117	-0.0088	0.00973	0.08444	0.02594
Uzbekistan	0.06279	0.02769	0.00212	-0.0122	0.07277	0.00919
Kyrgyzstan	0.10012	0.06862	-0.0084	0.03333	0.10988	0.03553
Tajikistan	0.06176	0.04496	0.02	0.01579	0.08588	0.02001
Turkmenistan	0.0746	0.02798	0.01686	-0.0067	0.07949	0.01462
Pakistan	0.11068	0.07963	0.06715	0.06324	0.07834	0.05411
Tibet	0.22438	0.23037	0.07911	0.18324	0.23566	0.17076
Afghanistan	0.11157	0.04831	0.06089	0.01091	0.10495	0.03329
India	0.38382	0.2774	0.17826	0.38396	0.365	0.29582
Nepal	0.14086	0.12897	0.02766	0.12614	0.20114	0.11012
AltaianKazakh	0.12719	0.02207	0.05138	-0.0037	0.03584	0.00603
AltaianKizhi	0.16853	0.16591	0.05008	0.10648	0.20819	0.11375
Buryat	0.14956	0.12337	0.03069	0.1036	0.18583	0.0819
Ket	0.14096	0.16069	-0.0132	0.11799	0.1974	0.10507
Khamnigan	0.15526	0.14479	0.02075	0.10668	0.19232	0.09434
Shor	0.12518	0.10851	0.00221	0.06918	0.12214	0.0586
Teleut	0.1143	0.13737	0.00767	0.09843	0.1965	0.07806
Tofalar	0.11533	0.15721	0.06298	0.06712	0.19094	0.0972
Tubular	0.09347	0.10368	0.00884	0.0331	0.08952	0.03176
Tuvinian	0.17762	0.14108	-0.0094	0.12302	0.17944	0.10446
Uyghur	0.11286	0.2012	-0.0455	0.1431	0.24523	0.12399
Evenki	0.23848	0.22175	0.07171	0.20445	0.26883	0.17827
Mansi	0.08628	0.08516	-0.0379	0.04974	0.10149	0.01801
Nganasan	0.19798	0.17462	0.0296	0.1801	0.21875	0.11663
Yakut	0.06855	0.10338	0.01278	0.04156	0.17235	0.07319
Chukchi	0.38026	0.32884	0.25579	0.36179	0.36095	0.32411
Even	0.23645	0.19081	0.06452	0.22428	0.26614	0.16316
Koryak	0.20378	0.18343	0.10862	0.19636	0.27386	0.15052
Negidal	0.0941	0.13378	-0.0322	0.06419	0.16987	0.0814
Nivkhi	0.25247	0.21237	0.31996	0.30006	0.31681	0.23503
Udegey	0.2676	0.20974	0.15439	0.24166	0.27809	0.19666
Ulchi	0.13002	0.12141	0.06713	0.11571	0.20896	0.09807
Yukaghir	0.26887	0.23417	0.10293	0.24818	0.30729	0.20233
Bargut	0.1717	0.14123	-0.007	0.12687	0.17593	0.10254
Han	0.16906	0.17114	0.07505	0.11368	0.19624	0.11633
Mongolia	0.04762	0.07261	-0.0403	0.0482	0.1361	0.02311

Population	Estonia	Hungary	Kalmyk	Moldova	Slovakia	Tatar
China	0.11014	0.08922	0.01275	0.03562	0.12387	0.06078

Population	Csango	Roma	Szekely	NorthOs	Adygei	Dargin
Iraq	0.01706	0.07	0.00657	0.03018	-0.0092	-0.0556
Kuwait	0.0218	0.0612	0.01693	0.00961	-0.0022	-0.0375
Iran	0.12157	0.1771	0.11589	0.06413	0.15535	0.1407
Turkey	0.04221	0.1198	0.03235	0.02352	0.0077	-0.0002
Cyprus	0.01432	0.0861	0.01745	0.05986	0.00043	-0.0277
Israel	0.01419	0.091	0.03392	0.00293	0.00156	0.02207
Palestine	0.09771	0.1726	0.06862	0.09271	0.06527	0.04343
Dubai	0.06668	0.058	0.06374	-0.018	0.02307	0.03857
Yemen	0.10122	0.1052	0.11734	0.02901	0.06045	0.10801
Jordan	0.05046	0.0942	0.04404	0.03604	0.02092	0.04644
Lebanon	0.06521	0.1483	0.05803	0.09185	-0.0204	0.09654
SaudiArabia	0.07807	0.0992	0.06725	0.03549	0.02768	0.00274
Syria	0.10211	0.226	0.13477	0.0644	0.15275	0.18134
Albania	0.0209	0.1069	0.03386	-0.01	-0.0019	0.00527
Romania	0.12873	0.2074	0.12977	0.09494	0.17357	0.12444
Bosnia	-0.0322	0.0783	-0.0323	-0.0136	-0.0816	0.01457
Belarus	0.10224	0.189	0.09454	0.12008	-0.0191	0.1699
Lithuania	0.05285	0.0929	0.0493	-0.0108	0.01129	0.00975
Russia	0.03901	0.0965	0.00418	0.09934	0.03214	-0.0567
Ukraine	0.06341	0.1014	0.06034	0.01421	0.06762	0.06948
Poland	0.08599	0.1297	0.05682	0.07507	0.05633	0.01245
Bulgaria	0.03158	0.0666	0.00165	0.03991	0.02447	-0.0129
Chuvash	0.22432	0.26	0.22706	0.14789	0.10743	0.22324
CzechRepublic	0.04967	0.1177	0.02126	0.08173	0.02744	-0.03
Estonia	0.05566	0.1222	0.05	-0.0054	0.05087	0.10264
Hungary	0.02718	0.0803	0.00109	0.06764	0.02601	-0.0425
Kalmyk	0.07912	0.074	0.07584	-0.0008	0.04631	0.09663
Moldova	-0.0066	0.0523	-0.0351	-0.0148	-0.0092	-0.0223
Slovakia	0.08044	0.1564	0.05719	0.11636	0.0783	0.03786
Tatar	0.02564	0.0662	0.00281	0.02348	-0.0192	-0.0207
Csango	0	0.0984	0.02495	0.04536	0.02506	0.01332
Roma	0.09839	0	0.06877	0.05645	0.09675	0.07691

Population	Csango	Roma	Szekely	NorthOs	Adygei	Dargin
Szekely	0.02495	0.0688	0	0.05509	0.00566	-0.0514
NorthOssetian	0.04536	0.0565	0.05509	0	0.0003	0.03622
Adygei	0.02506	0.0968	0.00566	0.0003	0	0.09574
Dargin	0.01332	0.0769	-0.0514	0.03622	0.09574	0
Armenia	0.01623	0.0572	-0.0012	0.00807	-0.0178	-0.0179
Azerbaijan	0.05269	0.1122	0.0328	0.03768	0.0181	0.04109
Georgia	0.02417	0.1076	0.02035	0.06443	-0.0004	0.00141
Kazakhstan	0.05098	0.0632	0.04174	0.04195	0.01898	-0.0022
Uzbekistan	0.03289	0.0463	0.02205	0.03077	0.00697	-0.0218
Kyrgyzstan	0.06817	0.0535	0.05519	0.04349	0.02969	0.03833
Tajikistan	0.04615	0.0569	0.03282	0.03073	-0.0068	0.00991
Turkmenistan	0.03638	0.0551	0.02087	0.03579	0.02523	-0.0136
Pakistan	0.04083	0.167	0.06024	0.06588	0.02695	0.10893
Tibet	0.19834	0.1896	0.20087	0.14157	0.19011	0.20295
Afghanistan	0.04108	0.0936	0.04701	0.06902	0.01536	0.00054
India	0.25755	0.2377	0.2442	0.22868	0.38614	0.48133
Nepal	0.11389	0.0593	0.10703	0.06339	0.1463	0.17639
AltaianKazakh	0.04375	0.1005	0.01371	0.06535	0.01505	-0.0605
AltaianKizhi	0.14239	0.0798	0.12884	0.08242	0.11642	0.14583
Buryat	0.11984	0.0702	0.09099	0.06833	0.0796	0.1302
Ket	0.08503	0.1037	0.12481	0.02757	0.11403	0.18889
Khamnigan	0.1284	0.0868	0.10796	0.07664	0.0924	0.12979
Shor	0.09212	0.0805	0.07952	0.06472	0.06239	0.04837
Teleut	0.12513	0.0476	0.09945	0.04915	0.10315	0.1326
Tofalar	0.12781	0.1079	0.11517	0.05054	0.06617	0.13934
Tubular	0.09025	0.1176	0.08644	0.06791	-0.0132	0.0074
Tuvinian	0.12813	0.1097	0.11576	0.07962	0.12028	0.15618
Uyghur	0.15024	0.1182	0.14722	-0.03	0.14391	0.36612
Evenki	0.20148	0.13	0.18145	0.1373	0.2066	0.23582
Mansi	0.07438	0.0877	0.0658	0.0344	0.02842	0.04958
Nganasan	0.15491	0.0908	0.13762	0.09658	0.1687	0.21546
Yakut	0.09415	0.0704	0.07383	0.03368	0.06533	0.12828
Chukchi	0.28882	0.2919	0.291	0.27494	0.3416	0.39776
Even	0.17016	0.1083	0.15835	0.11925	0.244	0.28377
Koryak	0.16846	0.0872	0.14645	0.11596	0.19259	0.22715
Negidal	0.12251	0.0887	0.10258	0.0316	0.0537	0.07244

Population	Csango	Roma	Szekely	NorthOs	Adygei	Dargin
Nivkhi	0.1939	0.2297	0.18819	0.22361	0.29674	0.36292
Udegey	0.1822	0.1365	0.17511	0.16953	0.27157	0.29388
Ulchi	0.10283	0.0774	0.09176	0.07087	0.10455	0.14935
Yukaghir	0.21347	0.1346	0.19499	0.15503	0.2554	0.29459
Bargut	0.12575	0.0997	0.11332	0.07009	0.11073	0.17157
Han	0.13683	0.1435	0.1436	0.09731	0.10985	0.14929
Mongolia	0.0351	0.0636	0.05954	0.00072	0.04078	0.05849
China	0.08554	0.0709	0.07839	0.05008	0.01764	0.06496

Population	Armenia	Azerbaijan	Georgia	Kazakhstan	Uzbekistan	Kyrgyzstan
Iraq	-0.0097	0.01314	0.00465	0.03818	0.01923	0.0518
Kuwait	-0.005	0.01712	0.01913	0.03033	0.01797	0.04001
Iran	0.09632	0.03416	0.1147	0.14864	0.1241	0.16201
Turkey	0.00834	-0.01413	0.01423	0.05416	0.04191	0.07579
Cyprus	0.00018	0.0451	0.00945	0.05195	0.02992	0.06734
Israel	0.00477	0.01151	0.02435	0.05919	0.03816	0.07196
Palestine	0.05462	0.08037	0.09623	0.08528	0.0795	0.11423
Dubai	0.02922	0.06961	0.08426	0.06496	0.04856	0.06817
Yemen	0.08466	0.12627	0.11458	0.10778	0.08695	0.10339
Jordan	0.0252	0.05031	0.0417	0.0403	0.02713	0.05646
Lebanon	0.03025	0.06706	0.05186	0.06969	0.05647	0.08597
SaudiArabia	0.01494	0.04585	0.04558	0.05617	0.04859	0.06333
Syria	0.09259	0.10511	0.10906	0.12826	0.12036	0.15508
Albania	-0.0091	0.01959	0.03089	0.04	0.02549	0.0532
Romania	0.10593	0.10595	0.1539	0.14154	0.13233	0.1597
Bosnia	-0.0825	-0.02666	-0.0624	0.0043	-0.013	0.02308
Belarus	0.09151	0.10751	0.10982	0.11073	0.10472	0.1272
Lithuania	0.01144	0.03413	0.0622	0.07142	0.04872	0.07506
Russia	0.01455	0.06408	0.03001	0.06139	0.0391	0.08171
Ukraine	0.0325	0.05671	0.09345	0.07183	0.06136	0.07702
Poland	0.06197	0.09543	0.09488	0.06043	0.05961	0.08516
Bulgaria	-0.0023	0.00982	0.0124	0.05422	0.02436	0.06443
Chuvash	0.18803	0.21835	0.21337	0.2266	0.20882	0.21496
CzechRepublic	0.02262	0.06717	0.02274	0.04708	0.03635	0.0716
Estonia	0.03465	-0.01252	0.07454	0.08574	0.06279	0.10012

Population	Armenia	Azerbaijan	Georgia	Kazakhstan	Uzbekistan	Kyrgyzstan
Hungary	0.00439	0.03692	0.01935	0.05117	0.02769	0.06862
Kalmyk	0.04484	0.09663	0.08316	-0.00875	0.00212	-0.00841
Moldova	-0.0512	0.00754	-0.0059	0.00973	-0.01222	0.03333
Slovakia	0.06561	0.10249	0.06534	0.08444	0.07277	0.10988
Tatar	-0.013	0.02541	-0.0051	0.02594	0.00919	0.03553
Csango	0.01623	0.05269	0.02417	0.05098	0.03289	0.06817
Roma	0.05718	0.11217	0.10756	0.06324	0.04632	0.0535
Szekely	-0.0012	0.0328	0.02035	0.04174	0.02205	0.05519
NorthOssetian	0.00807	0.03768	0.06443	0.04195	0.03077	0.04349
Adygei	-0.0178	0.0181	-0.0004	0.01898	0.00697	0.02969
Dargin	-0.0179	0.04109	0.00141	-0.00223	-0.02181	0.03833
Armenia	0	0.00526	-0.0087	0.03071	0.01118	0.03823
Azerbaijan	0.00526	0	0.01297	0.07139	0.04868	0.08663
Georgia	-0.0087	0.01297	0	0.05104	0.0301	0.06714
Kazakhstan	0.03071	0.07139	0.05104	0	0.00505	0.00636
Uzbekistan	0.01118	0.04868	0.0301	0.00505	0	0.00972
Kyrgyzstan	0.03823	0.08663	0.06714	0.00636	0.00972	0
Tajikistan	0.02282	0.04547	0.04239	0.02453	0.01478	0.02502
Turkmenistan	0.00639	0.05501	0.03444	0.00794	0.0026	0.01401
Pakistan	0.04562	0.06713	0.0384	0.05328	0.04643	0.08467
Tibet	0.17727	0.22163	0.21007	0.10267	0.12434	0.10754
Afghanistan	0.02717	0.07461	0.02827	0.05397	0.03742	0.06789
India	0.28707	0.33301	0.3425	0.11505	0.14715	0.11285
Nepal	0.099	0.1446	0.14022	0.04618	0.04298	0.02964
AltaianKazakh	-0.0008	0.06484	0.0096	0.02617	0.01849	0.04972
AltaianKizhi	0.10547	0.16802	0.15358	0.06892	0.06694	0.03774
Buryat	0.07276	0.13299	0.12455	0.03604	0.03996	0.0124
Ket	0.10795	0.14992	0.13658	0.01361	0.02998	0.02753
Khamnigan	0.0936	0.15131	0.13963	0.04004	0.04739	0.01624
Shor	0.06969	0.12072	0.08883	0.02985	0.0263	0.01844
Teleut	0.07518	0.12395	0.12086	0.05961	0.04849	0.0356
Tofalar	0.07752	0.12864	0.13019	0.07531	0.06899	0.04923
Tubular	0.05227	0.08821	0.05107	0.06154	0.05598	0.06185
Tuvinian	0.09328	0.15556	0.14496	0.02042	0.04101	0.0151
Uyghur	0.11209	0.16362	0.19928	0.04649	0.05295	0.03132
Evenki	0.17689	0.22901	0.22869	0.08245	0.09698	0.0567

Population	Armenia	Azerbaijan	Georgia	Kazakhstan	Uzbekistan	Kyrgyzstan
Mansi	0.04721	0.08256	0.05944	0.00781	0.01524	0.00907
Nganasan	0.13122	0.18699	0.17403	0.05423	0.06301	0.03423
Yakut	0.05029	0.08793	0.10975	0.02994	0.02522	0.00619
Chukchi	0.29483	0.34364	0.34184	0.18869	0.21503	0.20412
Even	0.164	0.21241	0.21519	0.05505	0.07111	0.03769
Koryak	0.14225	0.19444	0.19755	0.08765	0.08995	0.06119
Negidal	0.07019	0.11553	0.12665	0.01759	0.03637	0.02002
Nivkhi	0.18852	0.18567	0.21704	0.18541	0.16826	0.18252
Udegey	0.18249	0.23438	0.2289	0.10877	0.10665	0.08273
Ulchi	0.0766	0.11385	0.1216	0.04769	0.04277	0.02745
Yukaghir	0.20182	0.25217	0.2539	0.09694	0.11096	0.07162
Bargut	0.10313	0.15376	0.15085	0.01588	0.03562	0.00574
Han	0.11913	0.16771	0.14784	0.07746	0.08641	0.07585
Mongolia	0.0398	0.06983	0.05009	0.01959	0.00822	0.01429
China	0.0603	0.10095	0.08576	0.02792	0.03229	0.01716

Population	Tajikistan	Turkmenistan	Pakistan	Tibet	Afghanistan
Iraq	0.03087	0.01803	0.02702	0.17264	0.03074
Kuwait	0.02667	0.01529	0.02244	0.14343	0.04243
Iran	0.1197	0.13189	0.17084	0.28617	0.15593
Turkey	0.04832	0.04054	0.03188	0.17438	0.06285
Cyprus	0.04294	0.03356	0.04978	0.20181	0.01843
Israel	0.04031	0.04724	0.05043	0.18261	0.03577
Palestine	0.10309	0.08465	0.10551	0.23552	0.12959
Dubai	0.04393	0.05592	0.09117	0.17016	0.07927
Yemen	0.0913	0.10892	0.14419	0.20268	0.09561
Jordan	0.01918	0.03212	0.03464	0.17793	0.03446
Lebanon	0.0673	0.06964	0.09419	0.22982	0.06601
SaudiArabia	0.05562	0.05286	0.07539	0.07811	0.09169
Syria	0.14347	0.13172	0.1453	0.24495	0.11321
Albania	0.04721	0.03886	0.00917	0.1521	0.04032
Romania	0.15985	0.13507	0.17831	0.26208	0.18856
Bosnia	0.00012	-0.01087	-0.0048	0.13185	-0.00783
Belarus	0.10302	0.11654	0.13093	0.2693	0.14021
Lithuania	0.05812	0.05596	0.08575	0.18851	0.07813

Population	Tajikistan	Turkmenistan	Pakistan	Tibet	Afghanistan
Russia	0.05658	0.03861	0.0957	0.24908	0.05865
Ukraine	0.07693	0.06183	0.10914	0.18487	0.1156
Poland	0.07379	0.06441	0.08517	0.18129	0.11312
Bulgaria	0.02763	0.03149	0.07257	0.2197	0.04137
Chuvash	0.17653	0.23441	0.1831	0.32389	0.22919
CzechRepublic	0.05307	0.03879	0.0557	0.20258	0.0635
Estonia	0.06176	0.0746	0.11068	0.22438	0.11157
Hungary	0.04496	0.02798	0.07963	0.23037	0.04831
Kalmyk	0.02	0.01686	0.06715	0.07911	0.06089
Moldova	0.01579	-0.00669	0.06324	0.18324	0.01091
Slovakia	0.08588	0.07949	0.07834	0.23566	0.10495
Tatar	0.02001	0.01462	0.05411	0.17076	0.03329
Csango	0.04615	0.03638	0.04083	0.19834	0.04108
Roma	0.05687	0.05511	0.16697	0.18961	0.09358
Szekely	0.03282	0.02087	0.06024	0.20087	0.04701
NorthOssetian	0.03073	0.03579	0.06588	0.14157	0.06902
Adygei	-0.0068	0.02523	0.02695	0.19011	0.01536
Dargin	0.00991	-0.01361	0.10893	0.20295	0.00054
Armenia	0.02282	0.00639	0.04562	0.17727	0.02717
Azerbaijan	0.04547	0.05501	0.06713	0.22163	0.07461
Georgia	0.04239	0.03444	0.0384	0.21007	0.02827
Kazakhstan	0.02453	0.00794	0.05328	0.10267	0.05397
Uzbekistan	0.01478	0.0026	0.04643	0.12434	0.03742
Kyrgyzstan	0.02502	0.01401	0.08467	0.10754	0.06789
Tajikistan	0	0.01872	0.05218	0.14319	0.04939
Turkmenistan	0.01872	0	0.06293	0.14193	0.0456
Pakistan	0.05218	0.06293	0	0.2047	0.06328
Tibet	0.14319	0.14193	0.2047	0	0.19221
Afghanistan	0.04939	0.0456	0.06328	0.19221	0
India	0.1758	0.16694	0.40805	0.19985	0.25997
Nepal	0.05182	0.05272	0.18239	0.14027	0.10605
AltaianKazakh	0.04071	0.0194	0.04103	0.17423	0.03617
AltaianKizhi	0.06692	0.08071	0.16869	0.14701	0.13345
Buryat	0.04025	0.04672	0.13968	0.14175	0.10811
Ket	0.05537	0.0601	0.09416	0.02477	0.0764
Khamnigan	0.05124	0.05642	0.14792	0.12744	0.12719

Population	Tajikistan	Turkmenistan	Pakistan	Tibet	Afghanistan
Shor	0.03315	0.04264	0.08795	0.13186	0.08746
Teleut	0.04126	0.0653	0.14288	0.15388	0.10534
Tofalar	0.05053	0.08538	0.08826	0.14693	0.12417
Tubular	0.05007	0.06753	0.03688	0.08339	0.07386
Tuvinian	0.06807	0.05047	0.16243	0.06095	0.12676
Uyghur	0.04632	0.09311	0.16247	0.09568	0.14014
Evenki	0.10731	0.11548	0.2508	0.11958	0.1918
Mansi	0.03326	0.02094	0.06366	0.04654	0.07363
Nganasan	0.07348	0.0796	0.21118	0.10815	0.13542
Yakut	0.03578	0.03874	0.13247	0.13732	0.11006
Chukchi	0.24198	0.24297	0.35038	0.23671	0.29752
Even	0.09438	0.08604	0.26825	0.04977	0.16866
Koryak	0.08816	0.10108	0.24441	0.17817	0.15611
Negidal	0.04679	0.04836	0.10179	0.05558	0.11015
Nivkhi	0.1614	0.17996	0.30172	0.29239	0.22936
Udegey	0.11792	0.12584	0.26708	0.14133	0.19966
Ulchi	0.04204	0.04873	0.15884	0.14532	0.11254
Yukaghir	0.11745	0.1313	0.29737	0.16021	0.19051
Bargut	0.05698	0.04982	0.15143	0.10219	0.12185
Han	0.10132	0.10006	0.14916	-0.0003	0.13371
Mongolia	0.02083	0.02539	0.06147	0.12078	0.04167
China	0.03814	0.04002	0.09254	0.11694	0.07327

Population	India	Nepal	AltKazakh	AltKizhi	Buryat	Ket
Iraq	0.2143	0.0894	0.01167	0.11832	0.08272	0.08108
Kuwait	0.1687	0.0706	0.01895	0.09612	0.06338	0.04956
Iran	0.4042	0.1963	0.18445	0.22764	0.20355	0.21841
Turkey	0.2765	0.127	0.04221	0.14979	0.11162	0.08081
Cyprus	0.2642	0.1114	0.01942	0.1373	0.10793	0.10808
Israel	0.2941	0.0974	0.05995	0.12451	0.1042	0.07489
Palestine	0.3384	0.2273	0.06861	0.2004	0.16926	0.16976
Dubai	0.2925	0.0756	0.08404	0.09284	0.07375	0.05861
Yemen	0.2944	0.1201	0.135	0.12784	0.11914	0.09463
Jordan	0.3251	0.1002	0.03973	0.13174	0.09253	0.08431
Lebanon	0.3261	0.1918	0.06713	0.17944	0.14613	0.18934

Population	India	Nepal	AltKazakh	AltKizhi	Buryat	Ket
SaudiArabia	0.2144	0.0814	0.03784	0.09788	0.08684	0.03451
Syria	0.4326	0.2412	0.15801	0.22596	0.22861	0.15163
Albania	0.3165	0.1318	0.05541	0.10683	0.08519	0.01344
Romania	0.3389	0.2184	0.17241	0.22515	0.2097	0.1749
Bosnia	0.3645	0.115	-0.01754	0.10718	0.07886	0.06696
Belarus	0.3611	0.2335	0.12868	0.21896	0.18265	0.23095
Lithuania	0.2915	0.1108	0.07382	0.1249	0.10611	0.07216
Russia	0.3068	0.1608	0.00979	0.18567	0.14425	0.19049
Ukraine	0.2481	0.1091	0.09444	0.11719	0.09973	0.10286
Poland	0.2492	0.1482	0.04451	0.15682	0.13013	0.10749
Bulgaria	0.3555	0.1232	0.02554	0.14256	0.11323	0.15647
Chuvash	0.5151	0.2709	0.24729	0.18974	0.1633	0.20632
CzechRepublic	0.3123	0.1588	-0.01264	0.1689	0.13399	0.14984
Estonia	0.3838	0.1409	0.12719	0.16853	0.14956	0.14096
Hungary	0.2774	0.129	0.02207	0.16591	0.12337	0.16069
Kalmyk	0.1783	0.0277	0.05138	0.05008	0.03069	-0.0132
Moldova	0.384	0.1261	-0.00373	0.10648	0.1036	0.11799
Slovakia	0.365	0.2011	0.03584	0.20819	0.18583	0.1974
Tatar	0.2958	0.1101	0.00603	0.11375	0.0819	0.10507
Csango	0.2576	0.1139	0.04375	0.14239	0.11984	0.08503
Roma	0.2377	0.0593	0.10051	0.07983	0.07017	0.10371
Szekely	0.2442	0.107	0.01371	0.12884	0.09099	0.12481
NorthOssetian	0.2287	0.0634	0.06535	0.08242	0.06833	0.02757
Adygei	0.3861	0.1463	0.01505	0.11642	0.0796	0.11403
Dargin	0.4813	0.1764	-0.06046	0.14583	0.1302	0.18889
Armenia	0.2871	0.099	-0.00081	0.10547	0.07276	0.10795
Azerbaijan	0.333	0.1446	0.06484	0.16802	0.13299	0.14992
Georgia	0.3425	0.1402	0.0096	0.15358	0.12455	0.13658
Kazakhstan	0.1151	0.0462	0.02617	0.06892	0.03604	0.01361
Uzbekistan	0.1472	0.043	0.01849	0.06694	0.03996	0.02998
Kyrgyzstan	0.1129	0.0296	0.04972	0.03774	0.0124	0.02753
Tajikistan	0.1758	0.0518	0.04071	0.06692	0.04025	0.05537
Turkmenistan	0.1669	0.0527	0.0194	0.08071	0.04672	0.0601
Pakistan	0.4081	0.1824	0.04103	0.16869	0.13968	0.09416
Tibet	0.1999	0.1403	0.17423	0.14701	0.14175	0.02477
Afghanistan	0.26	0.1061	0.03617	0.13345	0.10811	0.0764

Population	India	Nepal	AltKazakh	AltKizhi	Buryat	Ket
India	0	0.2164	0.30296	0.20155	0.18183	0.27907
Nepal	0.2164	0	0.1418	0.04585	0.04754	0.08386
AltaianKazakh	0.303	0.1418	0	0.13836	0.10958	0.11716
AltaianKizhi	0.2016	0.0459	0.13836	0	0.00612	0.05727
Buryat	0.1818	0.0475	0.10958	0.00612	0	0.08864
Ket	0.2791	0.0839	0.11716	0.05727	0.08864	0
Khamnigan	0.1463	0.041	0.11735	-0.0067	-0.0267	0.06827
Shor	0.2135	0.0584	0.05693	0.00981	0.03184	0.04241
Teleut	0.3051	0.0351	0.12734	-0.0374	0.01598	0.03859
Tofalar	0.381	0.1098	0.13129	0.01377	0.00614	0.02051
Tubular	0.2365	0.0962	0.04427	0.0958	0.07317	0.02362
Tuvinian	0.0754	0.0653	0.09387	0.0781	0.04383	0.06271
Uyghur	0.3651	0.1048	0.15954	-0.0161	0.05876	-0.0721
Evenki	0.149	0.0902	0.19843	0.01134	0.05166	0.0723
Mansi	0.1962	0.0659	0.0457	0.068	0.04992	-0.0018
Nganasan	0.2323	0.0572	0.14699	-0.0042	0.04685	0.0373
Yakut	0.1781	0.0575	0.10913	-0.0023	0.00393	0.07835
Chukchi	0.3312	0.2998	0.31218	0.27048	0.26859	0.21387
Even	0.1745	0.0671	0.19704	0.05166	0.06693	0.06011
Koryak	0.2798	0.0654	0.19746	0.02771	0.03553	0.11499
Negidal	0.168	0.0636	0.06407	0.06518	0.03576	0.01923
Nivkhi	0.4773	0.2795	0.28186	0.27068	0.2395	0.35657
Udegey	0.283	0.1063	0.23532	0.04893	0.09184	0.13287
Ulchi	0.242	0.051	0.13519	0.04233	0.02784	0.07964
Yukaghir	0.204	0.1069	0.23519	0.02693	0.07024	0.07059
Bargut	0.0796	0.0597	0.11114	0.05258	0.02182	0.04101
Han	0.2335	0.1139	0.13236	0.11078	0.09485	-0.0103
Mongolia	0.2458	0.0236	0.06298	0.06164	0.05536	-0.0052
China	0.1141	0.0408	0.07414	0.05845	0.02144	0.0376

Population	Khamnigan	Shor	Teleut	Tofalar	Tubular	Tuvinian
Iraq	0.10134	0.0679	0.086	0.08738	0.06706	0.09714
Kuwait	0.07784	0.0527	0.06928	0.05908	0.06218	0.0712
Iran	0.21885	0.1903	0.16964	0.18509	0.16044	0.24333
Turkey	0.12538	0.0977	0.10072	0.09778	0.07026	0.12063

Population	Khamnigan	Shor	Teleut	Tofalar	Tubular	Tuvinian
Cyprus	0.1252	0.0894	0.11057	0.12244	0.08393	0.12384
Israel	0.11403	0.0852	0.07376	0.08874	0.06652	0.12589
Palestine	0.17364	0.1319	0.1916	0.16138	0.11905	0.14913
Dubai	0.08669	0.0874	0.0516	0.06184	0.0808	0.11898
Yemen	0.12512	0.1211	0.10382	0.12849	0.11324	0.16011
Jordan	0.11334	0.0934	0.09898	0.0981	0.04617	0.11869
Lebanon	0.15842	0.1325	0.18145	0.1867	0.1068	0.15222
SaudiArabia	0.08359	0.0569	0.0711	0.05665	0.04217	0.05952
Syria	0.22741	0.1761	0.20019	0.18673	0.12805	0.22223
Albania	0.09848	0.0583	0.07115	0.01012	0.03322	0.11048
Romania	0.20595	0.1821	0.20135	0.19826	0.17655	0.20404
Bosnia	0.09554	0.0497	0.08075	0.01732	-0.0178	0.09646
Belarus	0.1987	0.1865	0.21532	0.20551	0.1271	0.20373
Lithuania	0.11622	0.0883	0.08645	0.07228	0.07506	0.12152
Russia	0.16453	0.1224	0.16664	0.18268	0.11642	0.16155
Ukraine	0.10885	0.0931	0.09606	0.0957	0.10993	0.11596
Poland	0.13703	0.1019	0.15139	0.13097	0.10652	0.11246
Bulgaria	0.13093	0.0917	0.10232	0.13321	0.06656	0.15063
Chuvash	0.15445	0.1626	0.18919	0.04641	0.1347	0.29737
CzechRepublic	0.14358	0.0851	0.15409	0.15795	0.06472	0.1279
Estonia	0.15526	0.1252	0.1143	0.11533	0.09347	0.17762
Hungary	0.14479	0.1085	0.13737	0.15721	0.10368	0.14108
Kalmyk	0.02075	0.0022	0.00767	0.06298	0.00884	-0.0094
Moldova	0.10668	0.0692	0.09843	0.06712	0.0331	0.12302
Slovakia	0.19232	0.1221	0.1965	0.19094	0.08952	0.17944
Tatar	0.09434	0.0586	0.07806	0.0972	0.03176	0.10446
Csango	0.1284	0.0921	0.12513	0.12781	0.09025	0.12813
Roma	0.08676	0.0805	0.0476	0.10791	0.11764	0.10967
Szekely	0.10796	0.0795	0.09945	0.11517	0.08644	0.11576
NorthOssetian	0.07664	0.0647	0.04915	0.05054	0.06791	0.07962
Adygei	0.0924	0.0624	0.10315	0.06617	-0.0132	0.12028
Dargin	0.12979	0.0484	0.1326	0.13934	0.0074	0.15618
Armenia	0.0936	0.0697	0.07518	0.07752	0.05227	0.09328
Azerbaijan	0.15131	0.1207	0.12395	0.12864	0.08821	0.15556
Georgia	0.13963	0.0888	0.12086	0.13019	0.05107	0.14496
Kazakhstan	0.04004	0.0299	0.05961	0.07531	0.06154	0.02042

Population	Khamnigan	Shor	Teleut	Tofalar	Tubular	Tuvinian
Uzbekistan	0.04739	0.0263	0.04849	0.06899	0.05598	0.04101
Kyrgyzstan	0.01624	0.0184	0.0356	0.04923	0.06185	0.0151
Tajikistan	0.05124	0.0332	0.04126	0.05053	0.05007	0.06807
Turkmenistan	0.05642	0.0426	0.0653	0.08538	0.06753	0.05047
Pakistan	0.14792	0.088	0.14288	0.08826	0.03688	0.16243
Tibet	0.12744	0.1319	0.15388	0.14693	0.08339	0.06095
Afghanistan	0.12719	0.0875	0.10534	0.12417	0.07386	0.12676
India	0.1463	0.2135	0.30512	0.38098	0.23653	0.07541
Nepal	0.04102	0.0584	0.03513	0.10982	0.09618	0.06528
AltaianKazakh	0.11735	0.0569	0.12734	0.13129	0.04427	0.09387
AltaianKizhi	-0.00674	0.0098	-0.0374	0.01377	0.0958	0.0781
Buryat	-0.02669	0.0318	0.01598	0.00614	0.07317	0.04383
Ket	0.06827	0.0424	0.03859	0.02051	0.02362	0.06271
Khamnigan	0	0.0044	0.01456	0.02092	0.08372	0.03395
Shor	0.00439	0	0.00301	0.01006	0.01989	0.05213
Teleut	0.01456	0.003	0	-0.0004	0.05585	0.11002
Tofalar	0.02092	0.0101	-0.0004	0	0.01651	0.11809
Tubular	0.08372	0.0199	0.05585	0.01651	0	0.07359
Tuvinian	0.03395	0.0521	0.11002	0.11809	0.07359	0
Uyghur	0.03078	0.0255	-0.0563	-0.0433	0.04936	0.10019
Evenki	0.02674	0.0441	0.04031	0.09681	0.13295	0.05928
Mansi	0.0441	0.0108	0.04098	0.05042	-0.0124	0.01672
Nganasan	0.02431	0.011	-0.0224	0.06297	0.07347	0.06682
Yakut	0.00151	0.0085	0.00402	0.02737	0.07204	0.03957
Chukchi	0.23896	0.2478	0.3183	0.33443	0.25659	0.21676
Even	0.04278	0.0641	0.08242	0.13388	0.08778	0.02375
Koryak	0.03732	0.0732	0.02366	0.03898	0.12424	0.12306
Negidal	0.03409	0.0256	0.05628	0.04716	0.04041	-0.0045
Nivkhi	0.25204	0.247	0.29213	0.26399	0.17688	0.28168
Udegey	0.07206	0.0875	0.0685	0.10805	0.1357	0.13137
Ulchi	0.02757	0.043	0.0387	0.04253	0.06537	0.07887
Yukaghir	0.05568	0.0857	0.04912	0.1062	0.15033	0.10231
Bargut	0.02324	0.0435	0.08005	0.0958	0.08159	-0.0124
Han	0.09544	0.1032	0.11259	0.06969	0.04482	0.06773
Mongolia	0.05217	0.016	0.01967	0.05351	0.02952	0.05029
China	0.03628	0.0501	0.06945	0.05466	0.07347	0.02973

Population	Uyghur	Evenki	Mansi	Nganasan	Yakut	Chukchi	Even
Iraq	0.10405	0.16752	0.04659	0.12468	0.06465	0.2587	0.138
Kuwait	0.05781	0.13559	0.03013	0.1003	0.04396	0.2241	0.1079
Iran	0.2216	0.29183	0.14814	0.24921	0.14989	0.4154	0.2703
Turkey	0.10141	0.20058	0.04728	0.15745	0.07254	0.3044	0.1714
Cyprus	0.14333	0.19864	0.07644	0.14804	0.09664	0.2871	0.1729
Israel	0.05936	0.19309	0.06106	0.14082	0.06525	0.3062	0.172
Palestine	0.22374	0.24749	0.11235	0.23727	0.1216	0.3418	0.2545
Dubai	0.03092	0.17244	0.07037	0.11677	0.08397	0.2976	0.1598
Yemen	0.07697	0.2006	0.11723	0.15516	0.11521	0.3194	0.1878
Jordan	0.118	0.19665	0.07558	0.16568	0.10337	0.3468	0.1949
Lebanon	0.20341	0.23825	0.11289	0.20912	0.10926	0.3372	0.2474
SaudiArabia	0.05367	0.13355	0.01436	0.09049	0.06476	0.2627	0.0868
Syria	0.16748	0.28275	0.11687	0.25312	0.13465	0.4217	0.2918
Albania	-0.0219	0.16067	0.02311	0.1337	0.0031	0.3252	0.1578
Romania	0.20773	0.26606	0.13068	0.23248	0.12295	0.3585	0.2364
Bosnia	0.08846	0.18363	-0.0099	0.13144	0.02734	0.3279	0.1817
Belarus	0.2577	0.27865	0.13906	0.24564	0.14063	0.379	0.2807
Lithuania	0.04687	0.18583	0.0556	0.14131	0.04623	0.3111	0.1621
Russia	0.23867	0.2446	0.10576	0.19705	0.13273	0.3463	0.219
Ukraine	0.06426	0.16087	0.07047	0.12528	0.02764	0.2924	0.1428
Poland	0.12827	0.18923	0.09006	0.16817	0.10151	0.2781	0.1823
Bulgaria	0.19266	0.22418	0.07793	0.16496	0.10418	0.3541	0.2128
Chuvash	0.18947	0.32117	0.2071	0.31461	0.20753	0.4496	0.3727
CzechRepublic	0.19237	0.22703	0.06134	0.17602	0.13007	0.3225	0.2157
Estonia	0.11286	0.23848	0.08628	0.19798	0.06855	0.3803	0.2365
Hungary	0.2012	0.22175	0.08516	0.17462	0.10338	0.3288	0.1908
Kalmyk	-0.0455	0.07171	-0.0379	0.0296	0.01278	0.2558	0.0645
Moldova	0.1431	0.20445	0.04974	0.1801	0.04156	0.3618	0.2243
Slovakia	0.24523	0.26883	0.10149	0.21875	0.17235	0.361	0.2661
Tatar	0.12399	0.17827	0.01801	0.11663	0.07319	0.3241	0.1632
Csango	0.15024	0.20148	0.07438	0.15491	0.09415	0.2888	0.1702
Roma	0.11823	0.12998	0.08769	0.09076	0.07035	0.2919	0.1083
Szekely	0.14722	0.18145	0.0658	0.13762	0.07383	0.291	0.1584
NorthOssetian	-0.03	0.1373	0.0344	0.09658	0.03368	0.2749	0.1193

Population	Uyghur	Evenki	Mansi	Nganasan	Yakut	Chukchi	Even
Adygei	0.14391	0.2066	0.02842	0.1687	0.06533	0.3416	0.244
Dargin	0.36612	0.23582	0.04958	0.21546	0.12828	0.3978	0.2838
Armenia	0.11209	0.17689	0.04721	0.13122	0.05029	0.2948	0.164
Azerbaijan	0.16362	0.22901	0.08256	0.18699	0.08793	0.3436	0.2124
Georgia	0.19928	0.22869	0.05944	0.17403	0.10975	0.3418	0.2152
Kazakhstan	0.04649	0.08245	0.00781	0.05423	0.02994	0.1887	0.0551
Uzbekistan	0.05295	0.09698	0.01524	0.06301	0.02522	0.215	0.0711
Kyrgyzstan	0.03132	0.0567	0.00907	0.03423	0.00619	0.2041	0.0377
Tajikistan	0.04632	0.10731	0.03326	0.07348	0.03578	0.242	0.0944
Turkmenistan	0.09311	0.11548	0.02094	0.0796	0.03874	0.243	0.086
Pakistan	0.16247	0.2508	0.06366	0.21118	0.13247	0.3504	0.2683
Tibet	0.09568	0.11958	0.04654	0.10815	0.13732	0.2367	0.0498
Afghanistan	0.14014	0.1918	0.07363	0.13542	0.11006	0.2975	0.1687
India	0.36505	0.14904	0.19615	0.23226	0.17806	0.3312	0.1745
Nepal	0.1048	0.09021	0.06594	0.05718	0.05754	0.2998	0.0671
AltaianKazakh	0.15954	0.19843	0.0457	0.14699	0.10913	0.3122	0.197
AltaianKizhi	-0.0161	0.01134	0.068	-0.00418	-0.0023	0.2705	0.0517
Buryat	0.05876	0.05166	0.04992	0.04685	0.00393	0.2686	0.0669
Ket	-0.0721	0.0723	-0.0018	0.0373	0.07835	0.2139	0.0601
Khamnigan	0.03078	0.02674	0.0441	0.02431	0.00151	0.239	0.0428
Shor	0.02547	0.04406	0.01082	0.01098	0.00852	0.2478	0.0641
Teleut	-0.0563	0.04031	0.04098	-0.02237	0.00402	0.3183	0.0824
Tofalar	-0.0433	0.09681	0.05042	0.06297	0.02737	0.3344	0.1339
Tubular	0.04936	0.13295	-0.0124	0.07347	0.07204	0.2566	0.0878
Tuvinian	0.10019	0.05928	0.01672	0.06682	0.03957	0.2168	0.0238
Uyghur	0	0.02166	0.05064	0.00617	-0.0118	0.3627	0.1473
Evenki	0.02166	0	0.08343	0.00729	0.01007	0.2637	0.014
Mansi	0.05064	0.08343	0	0.02746	0.03368	0.2395	0.0321
Nganasan	0.00617	0.00729	0.02746	0	0.02792	0.2751	0.0129
Yakut	-0.0118	0.01007	0.03368	0.02792	0	0.2685	0.0533
Chukchi	0.36274	0.26367	0.23948	0.27513	0.2685	0	0.2765
Even	0.14729	0.01404	0.03214	0.0129	0.0533	0.2765	0
Koryak	0.11552	0.06805	0.10949	0.0428	0.05901	0.3035	0.0738
Negidal	-0.0165	0.06972	0.00521	0.03901	0.03184	0.2121	0.0554
Nivkhi	0.45148	0.32185	0.21917	0.33991	0.23338	0.446	0.3128
Udegey	0.14821	0.06184	0.1135	0.07059	0.0702	0.3087	0.0615

Population	Uyghur	Evenki	Mansi	Nganasan	Yakut	Chukchi	Even
Ulchi	0.12153	0.07166	0.04402	0.07304	0.02224	0.2897	0.0587
Yukaghir	0.04254	-0.0135	0.11921	0.00992	0.04634	0.3134	0.0381
Bargut	0.05263	0.03311	0.03488	0.05092	0.01187	0.2239	0.0338
Han	0.06759	0.11094	0.02882	0.09595	0.09788	0.2446	0.0492
Mongolia	-0.0335	0.11387	0.00622	0.06615	0.03757	0.2927	0.0898
China	0.04566	0.07612	0.03948	0.07309	0.02615	0.2077	0.0655

Population	Koryak	Negidal	Nivkhi	Udegey	Ulchi	Yukaghir	Bargut
Iraq	0.1359	0.08133	0.1566	0.1572	0.0775	0.17783	0.09579
Kuwait	0.1111	0.05234	0.1352	0.1323	0.0573	0.14605	0.06686
Iran	0.2357	0.18061	0.2413	0.2959	0.1689	0.30668	0.23674
Turkey	0.1732	0.08174	0.185	0.2086	0.1012	0.21963	0.12851
Cyprus	0.1618	0.11378	0.1986	0.1873	0.1073	0.21096	0.12591
Israel	0.1539	0.07844	0.1977	0.2	0.089	0.21228	0.12536
Palestine	0.2572	0.10562	0.2391	0.2955	0.1512	0.29782	0.15565
Dubai	0.1159	0.05621	0.2399	0.1909	0.08	0.1921	0.1161
Yemen	0.1698	0.1144	0.279	0.2074	0.1303	0.21518	0.14896
Jordan	0.1706	0.07909	0.26	0.2364	0.1087	0.21644	0.11004
Lebanon	0.2371	0.14555	0.2882	0.2666	0.1716	0.271	0.14639
SaudiArabia	0.1312	0.01387	0.1435	0.134	0.0608	0.1665	0.0857
Syria	0.285	0.16209	0.3432	0.3265	0.2042	0.30901	0.2163
Albania	0.1584	0.04176	0.2407	0.1793	0.0824	0.18529	0.09055
Romania	0.2502	0.16207	0.2844	0.2797	0.1822	0.28931	0.20348
Bosnia	0.152	0.0387	0.2074	0.1955	0.079	0.22394	0.09652
Belarus	0.253	0.18716	0.318	0.3021	0.2059	0.30536	0.19099
Lithuania	0.1551	0.05267	0.2207	0.2121	0.0905	0.20484	0.12093
Russia	0.2103	0.15581	0.2449	0.2338	0.1512	0.26192	0.16468
Ukraine	0.1406	0.06693	0.2243	0.1761	0.1009	0.17987	0.10597
Poland	0.2041	0.08874	0.2708	0.2189	0.1489	0.22268	0.10738
Bulgaria	0.1818	0.11051	0.2216	0.2235	0.1124	0.25115	0.15298
Chuvash	0.2826	0.1983	0.3411	0.338	0.2	0.36984	0.28767
CzechRepublic	0.2267	0.10914	0.2774	0.2465	0.1575	0.26258	0.13235
Estonia	0.2038	0.0941	0.2525	0.2676	0.13	0.26887	0.1717
Hungary	0.1834	0.13378	0.2124	0.2097	0.1214	0.23417	0.14123
Kalmyk	0.1086	-0.0322	0.32	0.1544	0.0671	0.10293	-0.007

Population	Koryak	Negidal	Nivkhi	Udegey	Ulchi	Yukaghir	Bargut
Moldova	0.1964	0.06419	0.3001	0.2417	0.1157	0.24818	0.12687
Slovakia	0.2739	0.16987	0.3168	0.2781	0.209	0.30729	0.17593
Tatar	0.1505	0.0814	0.235	0.1967	0.0981	0.20233	0.10254
Csango	0.1685	0.12251	0.1939	0.1822	0.1028	0.21347	0.12575
Roma	0.0872	0.08869	0.2297	0.1365	0.0774	0.1346	0.09965
Szekely	0.1465	0.10258	0.1882	0.1751	0.0918	0.19499	0.11332
NorthOssetian	0.116	0.0316	0.2236	0.1695	0.0709	0.15503	0.07009
Adygei	0.1926	0.0537	0.2967	0.2716	0.1046	0.2554	0.11073
Dargin	0.2272	0.07244	0.3629	0.2939	0.1494	0.29459	0.17157
Armenia	0.1423	0.07019	0.1885	0.1825	0.0766	0.20182	0.10313
Azerbaijan	0.1944	0.11553	0.1857	0.2344	0.1139	0.25217	0.15376
Georgia	0.1976	0.12665	0.217	0.2289	0.1216	0.2539	0.15085
Kazakhstan	0.0877	0.01759	0.1854	0.1088	0.0477	0.09694	0.01588
Uzbekistan	0.09	0.03637	0.1683	0.1067	0.0428	0.11096	0.03562
Kyrgyzstan	0.0612	0.02002	0.1825	0.0827	0.0275	0.07162	0.00574
Tajikistan	0.0882	0.04679	0.1614	0.1179	0.042	0.11745	0.05698
Turkmenistan	0.1011	0.04836	0.18	0.1258	0.0487	0.1313	0.04982
Pakistan	0.2444	0.10179	0.3017	0.2671	0.1588	0.29737	0.15143
Tibet	0.1782	0.05558	0.2924	0.1413	0.1453	0.16021	0.10219
Afghanistan	0.1561	0.11015	0.2294	0.1997	0.1125	0.19051	0.12185
India	0.2798	0.16797	0.4773	0.283	0.242	0.20396	0.07963
Nepal	0.0654	0.06355	0.2795	0.1063	0.051	0.10686	0.05974
AltaianKazakh	0.1975	0.06407	0.2819	0.2353	0.1352	0.23519	0.11114
AltaianKizhi	0.0277	0.06518	0.2707	0.0489	0.0423	0.02693	0.05258
Buryat	0.0355	0.03576	0.2395	0.0918	0.0278	0.07024	0.02182
Ket	0.115	0.01923	0.3566	0.1329	0.0796	0.07059	0.04101
Khamnigan	0.0373	0.03409	0.252	0.0721	0.0276	0.05568	0.02324
Shor	0.0732	0.02559	0.247	0.0875	0.043	0.08572	0.04345
Teleut	0.0237	0.05628	0.2921	0.0685	0.0387	0.04912	0.08005
Tofalar	0.039	0.04716	0.264	0.1081	0.0425	0.1062	0.0958
Tubular	0.1242	0.04041	0.1769	0.1357	0.0654	0.15033	0.08159
Tuvinian	0.1231	-0.0045	0.2817	0.1314	0.0789	0.10231	-0.0124
Uyghur	0.1155	-0.0165	0.4515	0.1482	0.1215	0.04254	0.05263
Evenki	0.0681	0.06972	0.3219	0.0618	0.0717	-0.0135	0.03311
Mansi	0.1095	0.00521	0.2192	0.1135	0.044	0.11921	0.03488
Nganasan	0.0428	0.03901	0.3399	0.0706	0.073	0.00992	0.05092

Population	Koryak	Negidal	Nivkhi	Udegey	Ulchi	Yukaghir	Bargut
Yakut	0.059	0.03184	0.2334	0.0702	0.0222	0.04634	0.01187
Chukchi	0.3035	0.21213	0.446	0.3087	0.2897	0.31341	0.22388
Even	0.0738	0.05535	0.3128	0.0615	0.0587	0.03807	0.03382
Koryak	0	0.0908	0.2742	0.0933	0.0379	0.05203	0.09914
Negidal	0.0908	0	0.261	0.1542	0.0511	0.11982	0.02684
Nivkhi	0.2742	0.26098	0	0.2699	0.1175	0.3692	0.29783
Udegey	0.0933	0.1542	0.2699	0	0.0579	0.09435	0.1232
Ulchi	0.0379	0.05111	0.1175	0.0579	0	0.09118	0.07081
Yukaghir	0.052	0.11982	0.3692	0.0944	0.0912	0	0.0606
Bargut	0.0991	0.02684	0.2978	0.1232	0.0708	0.0606	0
Han	0.1306	0.07146	0.2486	0.1083	0.096	0.13261	0.08796
Mongolia	0.0983	0.02195	0.2209	0.1264	0.0338	0.13446	0.05591
China	0.0779	0.03509	0.1853	0.1065	0.0432	0.08202	0.01244

Population	Han	Mongolia	China
Iraq	0.12199	0.03292	0.0719
Kuwait	0.10282	0.02078	0.0607
Iran	0.23966	0.11572	0.1743
Turkey	0.12283	0.0492	0.0939
Cyprus	0.14142	0.04747	0.0851
Israel	0.12689	0.00988	0.089
Palestine	0.19426	0.13114	0.1257
Dubai	0.11784	0.0161	0.08
Yemen	0.14127	0.04485	0.0996
Jordan	0.12541	0.04517	0.0528
Lebanon	0.1724	0.10793	0.088
SaudiArabia	0.05394	0.03215	0.0815
Syria	0.18959	0.1042	0.1496
Albania	0.07735	0.02213	0.0488
Romania	0.2232	0.14667	0.1808
Bosnia	0.05503	0.01759	0.0368
Belarus	0.21575	0.16655	0.1357
Lithuania	0.13258	0.03427	0.0885
Russia	0.18832	0.10823	0.1022
Ukraine	0.13926	0.06852	0.0947

Population	Han	Mongolia	China
Poland	0.14855	0.11014	0.091
Bulgaria	0.16409	0.05212	0.0873
Chuvash	0.24561	0.16621	0.1774
CzechRepublic	0.1567	0.08547	0.0889
Estonia	0.16906	0.04762	0.1101
Hungary	0.17114	0.07261	0.0892
Kalmyk	0.07505	-0.0403	0.0128
Moldova	0.11368	0.0482	0.0356
Slovakia	0.19624	0.1361	0.1239
Tatar	0.11633	0.02311	0.0608
Csango	0.13683	0.0351	0.0855
Roma	0.14345	0.06355	0.0709
Szekely	0.1436	0.05954	0.0784
NorthOssetian	0.09731	0.00072	0.0501
Adygei	0.10985	0.04078	0.0176
Dargin	0.14929	0.05849	0.065
Armenia	0.11913	0.0398	0.0603
Azerbaijan	0.16771	0.06983	0.101
Georgia	0.14784	0.05009	0.0858
Kazakhstan	0.07746	0.01959	0.0279
Uzbekistan	0.08641	0.00822	0.0323
Kyrgyzstan	0.07585	0.01429	0.0172
Tajikistan	0.10132	0.02083	0.0381
Turkmenistan	0.10006	0.02539	0.04
Pakistan	0.14916	0.06147	0.0925
Tibet	-0.0003	0.12078	0.1169
Afghanistan	0.13371	0.04167	0.0733
India	0.23351	0.24576	0.1141
Nepal	0.11392	0.02358	0.0408
AltaianKazakh	0.13236	0.06298	0.0741
AltaianKizhi	0.11078	0.06164	0.0585
Buryat	0.09485	0.05536	0.0214
Ket	-0.0103	-0.0052	0.0376
Khamnigan	0.09544	0.05217	0.0363
Shor	0.10317	0.01597	0.0501
Teleut	0.11259	0.01967	0.0695

Population	Han	Mongolia	China
Tofalar	0.06969	0.05351	0.0547
Tubular	0.04482	0.02952	0.0735
Tuvinian	0.06773	0.05029	0.0297
Uyghur	0.06759	-0.0335	0.0457
Evenki	0.11094	0.11387	0.0761
Mansi	0.02882	0.00622	0.0395
Nganasan	0.09595	0.06615	0.0731
Yakut	0.09788	0.03757	0.0262
Chukchi	0.24459	0.29266	0.2077
Even	0.04924	0.08977	0.0655
Koryak	0.13056	0.09833	0.0779
Negidal	0.07146	0.02195	0.0351
Nivkhi	0.24857	0.22091	0.1853
Udegey	0.10832	0.12639	0.1065
Ulchi	0.09604	0.03383	0.0432
Yukaghir	0.13261	0.13446	0.082
Bargut	0.08796	0.05591	0.0124
Han	0	0.07837	0.0769
Mongolia	0.07837	0	0.0324
China	0.07691	0.03236	0

APPENDIX C

TABLE OF CENTRAL ASIAN HAPLOGROUPS

Haplogroup	Kazakh	Kyrgyz	Tajik	Turkmen	Uzbek	N
A	2					2
A+152+16362	5	2	4		3	14
A+152+16362+16189		3			1	4
A+152+16362+200		1				1
A1a					1	1
A2r1				1		1
A5a	1					1
A8a		4			6	10
A8a1	4			3		7
A11	1			1	1	3
A12a		2			1	3
A14	1	1				2
A15	1					1
A16	1					1
A19	1					1
A23	1			2		3
A24	3	1		3		7
B4	1		1		1	3
B4+16261		4				4
B4a1c3	1	2				3
B4a1c3a				1	1	2
B4a2b	1					1
B4b1a1c			1			1
B4b1a3		2				2
B4b1a3a	1			1	1	3
B4b1b		1				1
B4b1b'c					1	1
B4c1b	1					1
B4c1b2b		4				4
B4c2		1				1
B4h		3				3
B4h1		3				3
B4m					1	1
B5b		1				1
B5b4		1				1

Haplogroup	Kazakh	Kyrgyz	Tajik	Turkmen	Uzbek	N
C	3	7		2	2	14
C4+152		1			1	2
C4+152+16093		1		6		7
C4a1					1	1
C4a1a+195	4	4	28		5	41
C4a1a3d	2	2			1	5
C4a1a4a	1	1			5	7
C4a1b		1				1
C4a2		1				1
C4a2a	1					1
C4a2a1	2			3	4	9
C4a2c		1				1
C4a2c1		3				3
C4b1		2	1	1	3	7
C4b2		1				1
C4b3			5	3		8
C4b8a					1	1
C4c1b					1	1
C4e	1		1		1	3
C5	1					1
C5a	4	3			1	8
C5a2				2		2
C5a2b		1				1
C5b1		2	1		1	4
C5b1b	1	1				2
C7+16051					1	1
D2b					1	1
D4+195		1				1
D4a					2	2
D4a+16294			1			1
D4a3	1	3			1	5
D4b1		1				1
D4b1a1	2			5		7
D4b1a2a1	3	2		2	2	9
D4b1b					1	1
D4b1c	1					1
D4b2a2a		1	7			8
D4b2b		4	1		2	7
D4b2d		1				1
D4c1a		1				1
D4c1b	2					2

Haplogroup	Kazakh	Kyrgyz	Tajik	Turkmen	Uzbek	N
D4c2a	3	4		3	2	12
D4c2b	1	2				3
D4e1a1					1	1
D4e1a2a	1					1
D4e2a		1	6			7
D4e5a	1				1	2
D4g1				4		4
D4g2a		2		1	1	4
D4h1	3				2	5
D4h2	2					2
D4i	3	3			2	8
D4I2		1		4		5
D4j					1	1
D4j+(16286)	1	1			1	3
D4j+146		1		1	1	3
D4j1a		1				1
D4j1b2	1					1
D4j2	1					1
D4j3		4			1	5
D4m2	1					1
D4m2a	1				1	2
D4n	1					1
D4n2					1	1
D4o1	1				2	3
D4o2a	4	1			1	6
D4q	1				1	2
D4s					1	1
D5		1				1
D5a2					2	2
D5a2a+16092		2				2
D5a2a1	1	2			2	5
D5a2a1+@16172		1		2	1	4
D5b	2	2			1	5
D5b1a1		1				1
D5b1b1					1	1
D5c1a		1	10			11
F	1		6		2	9
F1a1	4					4
F1a1a					1	1
F1a2					1	1
F1a3+16311					1	1

Haplogroup	Kazakh	Kyrgyz	Tajik	Turkmen	Uzbek	N
F1b1+@152	3	3	19	10	2	37
F1b1b	2	1	4		1	8
F1c1a1					1	1
F1d				1		1
F2a	1	1		1		3
F2b1		1				1
G1a1	1	1		5		7
G1a3	1					1
G2a	1					1
G2a+152	7	3		2	5	17
G2a1+16189				2		2
G2a2a	3	2			1	6
G2a5	3	1	1			5
G2b1b	2				1	3
G2b2b					1	1
G3a1					1	1
G3a3					1	1
H1+152		1		1		2
H1+16189	1			1		2
H1a					1	1
H1af					1	1
H1ag1a					1	1
H1aj1	1					1
H1as1a					1	1
H1b	1	2				3
H1b1+16362	2					2
H1b1g				1		1
H1b2					1	1
H1c	3			4	5	12
H1e+16129	1					1
H1e1a1		1	1			2
H1e1a3					2	2
H1e1a4					2	2
H1e1a6					1	1
H1e1b	1					1
H1e2c				4		4
H1j8	1					1
H1m1		1		1	1	3
H1n+146+195		1	2			3
H2a+152					1	1
H2a+152 16311	1	1		3	3	8

Haplogroup	Kazakh	Kyrgyz	Tajik	Turkmen	Uzbek	N
H2a1	2			6		8
H2a1f	1					1
H2a2a	6	3		13	7	29
H2a2a1			1			1
H2a5a1			4			4
H2a5b1					1	1
H3ak				1		1
H3h2	1					1
H3v		2				2
H5	1	1	5	2	1	10
H5+16192	1					1
H5+16311					1	1
H5a4				2	1	3
H5a5	1					1
H6	2				4	6
H6a1b1				7		7
H6a1b3	1					1
H6b			2			2
H6b2	2				1	3
H7a1					1	1
H7h		2				2
H10+(16093)	1					1
H11		2				2
H11a2		1				1
H13a1a1d				2		2
H13a1a2a					1	1
H13c2				1		1
H14a	1		1			2
H14b1	1				1	2
H15	2	1			4	7
H15a1a1			12			12
H15a1b					2	2
H20a					1	1
H26a1a1					1	1
H28				1	1	2
H33c					2	2
H41a					1	1
H57					1	1
H101				5	1	6
H107				2		2
HV0	3				2	5

Haplogroup	Kazakh	Kyrgyz	Tajik	Turkmen	Uzbek	N
HV0+195					1	1
HV1	1					1
HV1a1		2	1		1	4
HV2					1	1
HV2a	3				1	4
HV4b	1					1
HV6	1		1		2	4
HV14	1	1	3		2	7
HV15					1	1
HV17					1	1
HV19				2	1	3
I	1	1		3	1	6
I1		2			2	4
I1a1				1	2	3
I1c1					1	1
I1d					1	1
I4a1	1				2	3
J1	1					1
J1b	1			2	2	5
J1b1a1	4	1			1	6
J1b1a1+146		4		2		6
J1b1b					1	1
J1b3			1	11		12
J1b7			1			1
J1c			1		2	3
J1c2					2	2
J1c2i					1	1
J1c8a				2	1	3
J1d	1			1		2
J1d2					2	2
J2b		1				1
J2b1a	1	1		1		3
K1a	3	1			1	5
K1a+150			3		2	5
K1a1				1	1	2
K1a4a1c1	1					1
K1a4b				1	1	2
K1b2					1	1
K1c				5	1	6
K1c1e	1	1				2
K2					1	1

Haplogroup	Kazakh	Kyrgyz	Tajik	Turkmen	Uzbek	N
K2a5	1		1		2	4
K3					1	1
L1b1a1'4					2	2
M		1			1	2
M3					1	1
M3a1+204		1		1		2
M3c+152				1		1
M3d	1				1	2
M4a					1	1
M4b				1		1
M5a2a1a				2		2
M5a2a1a2		5				5
M7b1a1+(16192)	1					1
M7b1a1a1		1			1	2
M7b1a1c		1				1
M7b1a2a		2			1	3
M7b1b	1			1		2
M7c1					4	4
M7c1a1b			3			3
M8a2'3	1					1
M8a2a1	1	1				2
M8a3a		1				1
M9	5	11		1	4	21
M9a1a1a	2					2
M9a1b1				1		1
M9a'b	1				1	2
M10			3			3
M10a1+16129		2				2
M10a2	2					2
M11			1			1
M11+200			1			1
M13'46'61+16362	1	1		4	2	8
M13a1b		1				1
M18a		1				1
M30				2		2
M30+16234			1			1
M30c1		1	1			2
M33a1b			4	1		5
M33a2'3		1				1
M35a					1	1
M36	1				1	2

Haplogroup	Kazakh	Kyrgyz	Tajik	Turkmen	Uzbek	N
M37+152+151	1	1		1		3
M38a					1	1
M43a1	1	2		1	1	5
M45			1			1
M57a				4		4
M61					2	2
M64		1				1
M65a+@16311		1	1		2	4
M66b		1				1
M68				1		1
M71					1	1
N				6	5	11
N1a1a1a1a	1					1
N1a2			2			2
N1b1	1	1	1		3	6
N3					1	1
N9a	1				1	2
N9a1		1				1
N9a1'3	2	2				4
N9a5	1					1
N11a1		1				1
R0a+60. 1T	1				2	3
R0a1a				1		1
R0a2c					1	1
R1					2	2
R1b			1			1
R2	1	1		3	3	8
R5a1				1		1
R5a2					1	1
R5a2b					3	3
R9			1			1
R11				2		2
R11b1a				1		1
R30b1					1	1
T	1			7	2	10
T1		4	1			5
T1a		1	1		1	3
T1a+152					2	2
T1a13			1			1
T1a1'3	2		8	3	3	16
T1a1m	1		2			3

Haplogroup	Kazakh	Kyrgyz	Tajik	Turkmen	Uzbek	N
T2	1				3	4
T2a+195					2	2
T2a1b	1				1	2
T2b	2					2
T2b3+151				1		1
T2b34	2				4	6
T2c1f	1					1
T2d1		1	5		2	8
T2e					1	1
T2f1				2		2
T2f7a	1					1
T2g1	1					1
T2g1b			1			1
T2i					1	1
T3					1	1
U1a			7	2	1	10
U1a1a1	1					1
U1a1a+16129			1			1
U1a3	1				1	2
U1b2					1	1
U2a1a				2		2
U2b		1				1
U2b2	1					1
U2c'd	1					1
U2e1	3	1		3	6	13
U2e1'2'3	2		1		1	4
U2e1b1	1					1
U2e1h	1				1	2
U2e2			4	1	1	6
U3				2	2	4
U3a		1	4		1	6
U3b1a1		1				1
U3b2a1a					1	1
U3b3			1			1
U4	2	3			2	7
U4’9		1				1
U4a1		3		8		11
U4a1d					1	1
U4a2	2					2
U4a2b					1	1
U4b1a1a1		1	1			2

Haplogroup	Kazakh	Kyrgyz	Tajik	Turkmen	Uzbek	N
U4b1a3	1					1
U4b1b1b		2				2
U4b3	1					1
U4c1				1	1	2
U5a1		1				1
U5a1+@16192	3		14	2	1	20
U5a1a1+152			4		2	6
U5a1b1		2				2
U5a1g1					1	1
U5a1g2				1		1
U5a1h	1					1
U5a2	1					1
U5a2a	2	2				4
U5a2b1b	1					1
U5a2e					1	1
U5b1+16189					1	1
U5b1b1+@16192	1			1	4	6
U5b1c2			4		1	5
U5b1d1a					1	1
U5b1e	1					1
U5b2a1a		3			1	4
U5b2a1a2		1				1
U5b2a1b	2					2
U5b2a2	1					1
U5b2b1a	1					1
U7a	2	1	3		3	9
U7a1a				1		1
U7a3b				1	1	2
U7a4			9			9
U7a4a1					1	1
U8a		1				1
U8b1b	1					1
V+@72		1				1
V7b					1	1
W			14	2	1	17
W+194	1			1	2	4
W1+119					1	1
W1e1		2				2
W3a1+199					1	1
W3a2				1		1
W4	2					2

Haplogroup	Kazakh	Kyrgyz	Tajik	Turkmen	Uzbek	N
W4d				1		1
W6		2			1	3
X2		1		2		3
X2b+226					5	5
X2d				4		4
X2e2a2					1	1
X2i	1					1
Y		1				1
Y1		5		3	1	9
Z+152	2	2			1	5
Z1a	1				1	2
Z4a		1				1
	256	**249**	**244**	**249**	**328**	**1326**

APPENDIX D

TABLE OF HAPLOGROUP COUNTS AND PERCENTAGES

	Adygei		Dargin		North Ossetian		Armenia		Azerbaijan	
	N	%	N	%	N	%	N	%	N	%
Haplo-group	4	100.00	3	100.00	14	100.00	20	100.00	20	100.00
A	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
B	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
C	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
CZ	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
E	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
F	0	0.00	0	0.00	0	0.00	0	0.00	1	5.00
G	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
H	0	0.00	3	100.00	1	7.14	4	20.00	2	10.00
HV	0	0.00	0	0.00	0	0.00	1	5.00	1	5.00
I	0	0.00	0	0.00	2	14.29	0	0.00	0	0.00
J	0	0.00	0	0.00	4	28.57	3	15.00	2	10.00
JT	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
K	0	0.00	0	0.00	0	0.00	2	10.00	0	0.00
L0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L3	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M	0	0.00	0	0.00	1	7.14	0	0.00	0	0.00
M7	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N1	0	0.00	0	0.00	1	7.14	1	5.00	0	0.00
	Adygei		Dargin		North Ossetian		Armenia		Azerbaijan	

	N	%	N	%	N	%	N	%	N	%
N2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
P	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R	0	0.00	0	0.00	0	0.00	0	0.00	1	5.00
R0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
T	0	0.00	0	0.00	1	7.14	1	5.00	7	35.00
U1	1	25.00	0	0.00	0	0.00	1	5.00	2	10.00
U2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U3	1	25.00	0	0.00	0	0.00	2	10.00	1	5.00
U4	1	25.00	0	0.00	0	0.00	1	5.00	0	0.00
U5	1	25.00	0	0.00	0	0.00	0	0.00	0	0.00
U6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U7	0	0.00	0	0.00	0	0.00	0	0.00	2	10.00
U8	0	0.00	0	0.00	0	0.00	1	5.00	0	0.00
U9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
V	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
W	0	0.00	0	0.00	2	14.29	0	0.00	0	0.00
X2	0	0.00	0	0.00	2	14.29	3	15.00	1	5.00
X4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Y	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Z	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
	Georgia		**Kazakhstan**		**Kyrgyzstan**		**Tajikistan**		**Turkmenistan**	
	N	**%**	**N**	**%**	**N**	**%**	**N**	**%**	**N**	**%**
Haplo-group	20	100.00	256	100.00	249	100.00	244	100.00	249	100.00
A	0	0.00	21	8.20	14	5.62	4	1.64	10	4.02
B	0	0.00	6	2.34	21	8.43	2	0.82	2	0.80
C	0	0.00	20	7.81	32	12.85	36	14.75	17	6.83
CZ	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D4	0	0.00	35	13.67	35	14.06	15	6.15	20	8.03
D5	0	0.00	3	1.17	10	4.02	10	4.10	2	0.80
D6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
E	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
F	0	0.00	11	4.30	6	2.41	29	11.89	12	4.82
	Georgia		**Kazakhstan**		**Kyrgyzstan**		**Tajikistan**		**Turkmenistan**	

	N	%	N	%	N	%	N	%	N	%
G	0	0.00	18	7.03	8	3.21	1	0.41	9	3.61
H	5	25.00	35	13.67	19	7.63	28	11.48	57	22.89
HV	0	0.00	10	3.91	3	1.20	5	2.05	2	0.80
I	0	0.00	2	0.78	3	1.20	0	0.00	4	1.61
J	1	5.00	8	3.13	7	2.81	3	1.23	19	7.63
JT	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
K	3	15.00	6	2.34	2	0.80	4	1.64	7	2.81
L0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L3	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M	0	0.00	7	2.73	20	8.03	13	5.33	19	7.63
M7	0	0.00	2	0.78	4	1.61	3	1.23	1	0.40
M8	0	0.00	2	0.78	2	0.80	0	0.00	0	0.00
M9	0	0.00	8	3.13	11	4.42	0	0.00	2	0.80
N	0	0.00	0	0.00	1	0.40	0	0.00	6	2.41
N1	0	0.00	2	0.78	1	0.40	3	1.23	0	0.00
N2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N9	0	0.00	4	1.56	3	1.20	0	0.00	0	0.00
P	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R	2	10.00	1	0.39	1	0.40	1	0.41	7	2.81
R0	1	5.00	1	0.39	0	0.00	0	0.00	1	0.40
R9	0	0.00	0	0.00	0	0.00	1	0.41	0	0.00
T	3	15.00	13	5.08	6	2.41	19	7.79	13	5.22
U1	1	5.00	2	0.78	0	0.00	8	3.28	2	0.80
U2	0	0.00	9	3.52	2	0.80	5	2.05	6	2.41
U3	1	5.00	0	0.00	2	0.80	5	2.05	2	0.80
U4	3	15.00	6	2.34	10	4.02	1	0.41	9	3.61
U5	0	0.00	14	5.47	9	3.61	22	9.02	4	1.61
U6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U7	0	0.00	2	0.78	1	0.40	12	4.92	2	0.80
U8	0	0.00	1	0.39	1	0.40	0	0.00	0	0.00
U9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
V	0	0.00	0	0.00	1	0.40	0	0.00	0	0.00
	Georgia		**Kazakhstan**		**Kyrgyzstan**		**Tajikistan**		**Turkmenistan**	

	N	%	N	%	N	%	N	%	N	%
W	0	0.00	3	1.17	4	1.61	14	5.74	5	2.01
X2	0	0.00	1	0.39	1	0.40	0	0.00	6	2.41
X4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Y	0	0.00	0	0.00	6	2.41	0	0.00	3	1.20
Z	0	0.00	3	1.17	3	1.20	0	0.00	0	0.00
	Uzbekistan		**Bargut**		**China**		**Han**		**Mongolia**	
	N	**%**	**N**	**%**	**N**	**%**	**N**	**%**	**N**	**%**
Haplo-group	328	100.00	20	100.00	377	100.00	16	100.00	9	100.00
A	13	3.96	0	0.00	15	3.98	2	12.50	0	0.00
B	5	1.52	2	10.00	62	16.45	0	0.00	0	0.00
C	28	8.54	3	15.00	14	3.71	1	6.25	0	0.00
CZ	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D4	29	8.84	9	45.00	46	12.20	1	6.25	0	0.00
D5	7	2.13	1	5.00	20	5.31	0	0.00	1	11.11
D6	0	0.00	0	0.00	3	0.80	0	0.00	0	0.00
E	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
F	9	2.74	1	5.00	74	19.63	3	18.75	0	0.00
G	10	3.05	0	0.00	7	1.86	1	6.25	0	0.00
H	53	16.16	0	0.00	1	0.27	0	0.00	0	0.00
HV	13	3.96	0	0.00	1	0.27	0	0.00	0	0.00
I	9	2.74	0	0.00	0	0.00	0	0.00	0	0.00
J	12	3.66	0	0.00	1	0.27	0	0.00	0	0.00
JT	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
K	11	3.35	0	0.00	0	0.00	0	0.00	0	0.00
L0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L1	2	0.61	0	0.00	0	0.00	0	0.00	0	0.00
L2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L3	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M	15	4.57	1	5.00	19	5.04	2	12.50	1	11.11
M7	6	1.83	0	0.00	58	15.38	2	12.50	2	22.22
M8	0	0.00	0	0.00	5	1.33	0	0.00	0	0.00
M9	5	1.52	0	0.00	10	2.65	0	0.00	1	11.11
N	6	1.83	0	0.00	5	1.33	0	0.00	0	0.00
	Uzbekistan		**Bargut**		**China**		**Han**		**Mongolia**	

	N	%	N	%	N	%	N	%	N	%
N1	3	0.91	0	0.00	0	0.00	0	0.00	0	0.00
N2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N9	1	0.30	2	10.00	5	1.33	2	12.50	0	0.00
P	0	0.00	0	0.00	1	0.27	0	0.00	0	0.00
R	10	3.05	0	0.00	4	1.06	1	6.25	0	0.00
R0	3	0.91	0	0.00	0	0.00	0	0.00	0	0.00
R9	0	0.00	1	5.00	16	4.24	0	0.00	0	0.00
T	23	7.01	0	0.00	0	0.00	0	0.00	1	11.11
U1	3	0.91	0	0.00	0	0.00	0	0.00	0	0.00
U2	9	2.74	0	0.00	0	0.00	0	0.00	0	0.00
U3	4	1.22	0	0.00	0	0.00	0	0.00	0	0.00
U4	5	1.52	0	0.00	0	0.00	0	0.00	1	11.11
U5	13	3.96	0	0.00	0	0.00	0	0.00	0	0.00
U6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U7	5	1.52	0	0.00	0	0.00	0	0.00	0	0.00
U8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
V	1	0.30	0	0.00	0	0.00	0	0.00	0	0.00
W	6	1.83	0	0.00	0	0.00	0	0.00	1	11.11
X2	6	1.83	0	0.00	0	0.00	0	0.00	0	0.00
X4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Y	1	0.30	0	0.00	3	0.80	0	0.00	1	11.11
Z	2	0.61	0	0.00	7	1.86	1	6.25	0	0.00
	Albania		**Belarus**		**Bosnia**		**Bulgaria**		**Chuvash**	
	N	**%**	**N**	**%**	**N**	**%**	**N**	**%**	**N**	**%**
Haplo-group	5	100.00	20	100.00	5	100.00	20	100.00	4	100.00
A	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
B	0	0.00	0	0.00	0	0.00	0	0.00	3	75.00
C	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
CZ	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
E	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
F	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
	Albania		**Belarus**		**Bosnia**		**Bulgaria**		**Chuvash**	

	N	%	N	%	N	%	N	%	N	%
G	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
H	0	0.00	0	0.00	1	20.00	10	50.00	0	0.00
HV	0	0.00	0	0.00	1	20.00	0	0.00	0	0.00
I	0	0.00	0	0.00	0	0.00	1	5.00	1	25.00
J	2	40.00	3	15.00	1	20.00	0	0.00	0	0.00
JT	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
K	1	20.00	0	0.00	1	20.00	1	5.00	0	0.00
L0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L3	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M7	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N	1	20.00	0	0.00	0	0.00	0	0.00	0	0.00
N1	0	0.00	0	0.00	0	0.00	1	5.00	0	0.00
N2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
P	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R0	0	0.00	0	0.00	0	0.00	1	5.00	0	0.00
R9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
T	0	0.00	0	0.00	0	0.00	4	20.00	0	0.00
U1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U3	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U4	0	0.00	4	20.00	0	0.00	1	5.00	0	0.00
U5	0	0.00	13	65.00	1	20.00	0	0.00	0	0.00
U6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U7	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
V	1	20.00	0	0.00	0	0.00	0	0.00	0	0.00
W	0	0.00	0	0.00	0	0.00	1	5.00	0	0.00
	Albania		**Belarus**		**Bosnia**		**Bulgaria**		**Chuvash**	

	N	%	N	%	N	%	N	%	N	%
X2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
X4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Y	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Z	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
	Csango		**Czech Republic**		**Estonia**		**Hungary**		**Kalmyk**	
	N	**%**	**N**	**%**	**N**	**%**	**N**	**%**	**N**	**%**
Haplo-group	100	100.00	20	100.00	7	100.00	211	100.00	6	100.00
A	2	2.00	0	0.00	0	0.00	0	0.00	0	0.00
B	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
C	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
CZ	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D4	0	0.00	1	5.00	0	0.00	0	0.00	1	16.67
D5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
E	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
F	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
G	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
H	20	20.00	8	40.00	0	0.00	81	38.39	0	0.00
HV	2	2.00	3	15.00	0	0.00	11	5.21	0	0.00
I	2	2.00	0	0.00	0	0.00	6	2.84	0	0.00
J	14	14.00	0	0.00	2	28.57	21	9.95	0	0.00
JT	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
K	23	23.00	0	0.00	0	0.00	9	4.27	0	0.00
L0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L2	0	0.00	1	5.00	0	0.00	1	0.47	0	0.00
L3	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M	0	0.00	0	0.00	0	0.00	2	0.95	1	16.67
M7	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M9	0	0.00	0	0.00	0	0.00	2	0.95	2	33.33
N	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N1	4	4.00	0	0.00	0	0.00	2	0.95	0	0.00
	Csango		**Czech**		**Estonia**		**Hungary**		**Kalmyk**	

			Republic							
	N	%	N	%	N	N	%	N	%	N
N2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N9	0	0.00	1	5.00	0	0.00	0	0.00	0	0.00
P	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R0	1	1.00	0	0.00	0	0.00	2	0.95	0	0.00
R9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
T	5	5.00	1	5.00	3	42.86	30	14.22	0	0.00
U1	0	0.00	0	0.00	0	0.00	1	0.47	0	0.00
U2	2	2.00	0	0.00	0	0.00	3	1.42	0	0.00
U3	1	1.00	0	0.00	0	0.00	2	0.95	0	0.00
U4	2	2.00	5	25.00	0	0.00	8	3.79	1	16.67
U5	8	8.00	0	0.00	1	14.29	17	8.06	0	0.00
U6	0	0.00	0	0.00	0	0.00	1	0.47	0	0.00
U7	0	0.00	0	0.00	0	0.00	1	0.47	1	16.67
U8	4	4.00	0	0.00	0	0.00	1	0.47	0	0.00
U9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
V	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
W	9	9.00	0	0.00	1	14.29	6	2.84	0	0.00
X2	1	1.00	0	0.00	0	0.00	3	1.42	0	0.00
X4	0	0.00	0	0.00	0	0.00	1	0.47	0	0.00
Y	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Z	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
	Lithuania		**Moldova**		**Poland**		**Roma**		**Romania**	
	N	%	N	%	N	%	N	%	N	%
Haplo-group	12	100.00	4	100.00	20	100.00	205	100.00	17	100.00
A	0	0.00	0	0.00	1	5.00	0	0.00	0	0.00
B	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
C	0	0.00	0	0.00	1	5.00	0	0.00	0	0.00
CZ	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D5	0	0.00	0	0.00	1	5.00	0	0.00	0	0.00
D6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
E	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
F	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
G	0	0.00	0	0.00	1	5.00	0	0.00	0	0.00

	Lithuania		Moldova		Poland		Roma		Romania	
	N	%	N	%	N	%	N	%	N	%
H	1	8.33	2	50.00	12	60.00	34	16.59	0	0.00
HV	2	16.67	1	25.00	0	0.00	5	2.44	0	0.00
I	3	25.00	0	0.00	0	0.00	5	2.44	0	0.00
J	4	33.33	1	25.00	1	5.00	10	4.88	9	52.94
JT	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
K	0	0.00	0	0.00	0	0.00	3	1.46	0	0.00
L0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L1	0	0.00	0	0.00	1	5.00	0	0.00	0	0.00
L2	0	0.00	0	0.00	2	10.00	0	0.00	0	0.00
L3	0	0.00	0	0.00	0	0.00	1	0.49	0	0.00
L4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M	0	0.00	0	0.00	0	0.00	70	34.15	0	0.00
M7	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N	0	0.00	0	0.00	0	0.00	11	5.37	1	5.88
N1	0	0.00	0	0.00	0	0.00	2	0.98	1	5.88
N2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
P	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R0	0	0.00	0	0.00	0	0.00	0	0.00	5	29.41
R9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
T	2	16.67	0	0.00	0	0.00	14	6.83	1	5.88
U1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U2	0	0.00	0	0.00	0	0.00	2	0.98	0	0.00
U3	0	0.00	0	0.00	0	0.00	1	0.49	0	0.00
U4	0	0.00	0	0.00	0	0.00	1	0.49	0	0.00
U5	0	0.00	0	0.00	0	0.00	4	1.95	0	0.00
U6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U7	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
V	0	0.00	0	0.00	0	0.00	1	0.49	0	0.00
W	0	0.00	0	0.00	0	0.00	1	0.49	0	0.00
X2	0	0.00	0	0.00	0	0.00	40	19.51	0	0.00

	Lithuania		Moldova		Poland		Roma		Romania	
	N	%	N	%	N	%	N	%	N	%
X4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Y	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Z	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
	Russia		Slovakia		Szekely		Tatar		Ukraine	
	N	%	N	%	N	%	N	%	N	%
Haplo-group	151	100.00	20	100.00	178	100.00	20	100.00	20	100.00
A	0	0.00	0	0.00	2	1.12	0	0.00	0	0.00
B	0	0.00	0	0.00	1	0.56	0	0.00	0	0.00
C	0	0.00	0	0.00	9	5.06	0	0.00	2	10.00
CZ	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D4	0	0.00	0	0.00	0	0.00	1	5.00	0	0.00
D5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
E	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
F	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
G	0	0.00	0	0.00	1	0.56	0	0.00	1	5.00
H	73	48.34	11	55.00	62	34.83	3	15.00	4	20.00
HV	7	4.64	0	0.00	7	3.93	1	5.00	0	0.00
I	4	2.65	0	0.00	1	0.56	1	5.00	2	10.00
J	10	6.62	1	5.00	15	8.43	1	5.00	8	40.00
JT	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
K	7	4.64	0	0.00	8	4.49	1	5.00	0	0.00
L0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L2	0	0.00	2	10.00	0	0.00	0	0.00	0	0.00
L3	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M7	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N	0	0.00	0	0.00	1	0.56	0	0.00	0	0.00
N1	1	0.66	0	0.00	1	0.56	1	5.00	0	0.00
N2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00

	Russia		Slovakia		Szekely		Tatar		Ukraine	
	N	%	N	%	N	%	N	%	N	%
N9	0	0.00	0	0.00	0	0.00	1	5.00	0	0.00
P	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R	1	0.66	0	0.00	0	0.00	0	0.00	0	0.00
R0	0	0.00	0	0.00	4	2.25	0	0.00	0	0.00
R9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
T	10	6.62	0	0.00	17	9.55	1	5.00	2	10.00
U1	0	0.00	0	0.00	2	1.12	0	0.00	0	0.00
U2	3	1.99	0	0.00	3	1.69	0	0.00	0	0.00
U3	2	1.32	0	0.00	0	0.00	1	5.00	0	0.00
U4	6	3.97	6	30.00	6	3.37	4	20.00	0	0.00
U5	14	9.27	0	0.00	14	7.87	2	10.00	0	0.00
U6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U7	0	0.00	0	0.00	1	0.56	0	0.00	0	0.00
U8	2	1.32	0	0.00	6	3.37	0	0.00	0	0.00
U9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
V	6	3.97	0	0.00	3	1.69	1	5.00	0	0.00
W	3	1.99	0	0.00	9	5.06	1	5.00	1	5.00
X2	2	1.32	0	0.00	4	2.25	0	0.00	0	0.00
X4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Y	0	0.00	0	0.00	1	0.56	0	0.00	0	0.00
Z	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
	Cyprus		Dubai		Iran		Iraq		Israel	
	N	%	N	%	N	%	N	%	N	%
Haplo-group	91	100.00	12	100.00	20	100.00	182	100.00	16	100.00
A	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
B	0	0.00	0	0.00	0	0.00	3	1.65	0	0.00
C	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
CZ	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
E	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
F	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
G	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
H	29	31.87	0	0.00	0	0.00	41	22.53	0	0.00

	Cyprus		Dubai		Iran		Iraq		Israel	
	N	%	N	%	N	%	N	%	N	%
HV	1	1.10	0	0.00	1	5.00	16	8.79	1	6.25
I	3	3.30	1	8.33	1	5.00	3	1.65	0	0.00
J	5	5.49	1	8.33	6	30.00	21	11.54	2	12.50
JT	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
K	19	20.88	0	0.00	0	0.00	8	4.40	4	25.00
L0	0	0.00	0	0.00	0	0.00	2	1.10	0	0.00
L1	2	2.20	0	0.00	0	0.00	2	1.10	0	0.00
L2	1	1.10	0	0.00	0	0.00	5	2.75	0	0.00
L3	0	0.00	0	0.00	0	0.00	10	5.49	0	0.00
L4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M	2	2.20	0	0.00	0	0.00	2	1.10	1	6.25
M7	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N1	1	1.10	4	33.33	0	0.00	4	2.20	0	0.00
N2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
P	0	0.00	0	0.00	0	0.00	1	0.55	0	0.00
R	3	3.30	0	0.00	0	0.00	0	0.00	0	0.00
R0	0	0.00	1	8.33	0	0.00	3	1.65	0	0.00
R9	0	0.00	0	0.00	0	0.00	1	0.55	0	0.00
T	7	7.69	2	16.67	12	60.00	23	12.64	5	31.25
U1	2	2.20	0	0.00	0	0.00	6	3.30	0	0.00
U2	0	0.00	0	0.00	0	0.00	2	1.10	0	0.00
U3	5	5.49	0	0.00	0	0.00	7	3.85	0	0.00
U4	2	2.20	0	0.00	0	0.00	5	2.75	0	0.00
U5	2	2.20	0	0.00	0	0.00	4	2.20	0	0.00
U6	0	0.00	0	0.00	0	0.00	1	0.55	0	0.00
U7	1	1.10	0	0.00	0	0.00	5	2.75	0	0.00
U8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U9	0	0.00	0	0.00	0	0.00	2	1.10	0	0.00
V	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
W	3	3.30	1	8.33	0	0.00	2	1.10	2	12.50
X2	3	3.30	2	16.67	0	0.00	3	1.65	1	6.25
X4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00

	Cyprus		Dubai		Iran		Iraq		Israel	
	%	N	%	N	%	N	%	N	%	
Y	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Z	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
	Jordan		Kuwait		Lebanon		Palestine		Saudi Arabia	
	N	%	N	%	N	%	N	%	N	%
Haplo-group	12	100.00	381	100.00	20	100.00	9	100.00	18	100.00
A	0	0.00	1	0.26	0	0.00	0	0.00	0	0.00
B	0	0.00	4	1.05	0	0.00	0	0.00	0	0.00
C	0	0.00	2	0.52	0	0.00	0	0.00	0	0.00
CZ	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
E	0	0.00	1	0.26	0	0.00	0	0.00	0	0.00
F	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
G	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
H	2	16.67	71	18.64	0	0.00	0	0.00	0	0.00
HV	1	8.33	10	2.62	0	0.00	0	0.00	0	0.00
I	0	0.00	5	1.31	0	0.00	0	0.00	0	0.00
J	0	0.00	60	15.75	1	5.00	1	11.11	0	0.00
JT	0	0.00	1	0.26	0	0.00	0	0.00	0	0.00
K	0	0.00	10	2.62	1	5.00	1	11.11	1	5.56
L0	0	0.00	4	1.05	0	0.00	0	0.00	0	0.00
L1	0	0.00	3	0.79	0	0.00	0	0.00	0	0.00
L2	0	0.00	20	5.25	0	0.00	0	0.00	0	0.00
L3	1	8.33	8	2.10	0	0.00	0	0.00	0	0.00
L4	0	0.00	3	0.79	0	0.00	0	0.00	0	0.00
L5	0	0.00	1	0.26	0	0.00	0	0.00	0	0.00
M	2	16.67	22	5.77	0	0.00	0	0.00	7	38.89
M7	0	0.00	1	0.26	0	0.00	0	0.00	0	0.00
M8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N	0	0.00	6	1.57	0	0.00	0	0.00	0	0.00
N1	1	8.33	26	6.82	1	5.00	0	0.00	2	11.11
N2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00

	Jordan		Kuwait		Lebanon		Palestine		Saudi Arabia	
	N	%	N	%	N	%	N	%	N	%
P	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R	1	8.33	4	1.05	0	0.00	0	0.00	0	0.00
R0	0	0.00	31	8.14	2	10.00	5	55.56	7	38.89
R9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
T	1	8.33	26	6.82	0	0.00	0	0.00	1	5.56
U1	0	0.00	6	1.57	3	15.00	0	0.00	0	0.00
U2	2	16.67	4	1.05	0	0.00	0	0.00	0	0.00
U3	0	0.00	6	1.57	9	45.00	0	0.00	0	0.00
U4	0	0.00	5	1.31	0	0.00	0	0.00	0	0.00
U5	0	0.00	4	1.05	1	5.00	0	0.00	0	0.00
U6	0	0.00	3	0.79	1	5.00	2	22.22	0	0.00
U7	0	0.00	13	3.41	0	0.00	0	0.00	0	0.00
U8	1	8.33	3	0.79	1	5.00	0	0.00	0	0.00
U9	0	0.00	4	1.05	0	0.00	0	0.00	0	0.00
V	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
W	0	0.00	4	1.05	0	0.00	0	0.00	0	0.00
X2	0	0.00	8	2.10	0	0.00	0	0.00	0	0.00
X4	0	0.00	1	0.26	0	0.00	0	0.00	0	0.00
Y	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Z	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
	Syria		**Turkey**		**Yemen**		**Evenki**		**Mansi**	
	N	%	N	%	N	%	N	%	N	%
Haplo-group	6	100.00	20	100.00	19	100.00	19	100.00	12	100.00
A	0	0.00	2	10.00	0	0.00	1	5.26	1	8.33
B	0	0.00	1	5.00	0	0.00	0	0.00	0	0.00
C	0	0.00	0	0.00	0	0.00	9	47.37	1	8.33
CZ	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D4	0	0.00	0	0.00	0	0.00	5	26.32	3	25.00
D5	0	0.00	0	0.00	0	0.00	2	10.53	1	8.33
D6	0	0.00	0	0.00	0	0.00	1	5.26	0	0.00
E	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
F	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
G	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
H	0	0.00	2	10.00	0	0.00	0	0.00	1	8.33
HV	0	0.00	2	10.00	0	0.00	0	0.00	0	0.00

	Syria		Turkey		Yemen		Evenki		Mansi	
	N	%	N	%	N	%	N	%	N	%
I	0	0.00	0	0.00	7	36.84	0	0.00	0	0.00
J	3	50.00	4	20.00	3	15.79	0	0.00	1	8.33
JT	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
K	2	33.33	0	0.00	3	15.79	0	0.00	0	0.00
L0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L3	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M7	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N1	0	0.00	0	0.00	1	5.26	0	0.00	0	0.00
N2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
P	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R0	1	16.67	0	0.00	0	0.00	0	0.00	0	0.00
R9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
T	0	0.00	5	25.00	0	0.00	0	0.00	0	0.00
U1	0	0.00	1	5.00	0	0.00	0	0.00	0	0.00
U2	0	0.00	1	5.00	0	0.00	0	0.00	0	0.00
U3	0	0.00	0	0.00	2	10.53	0	0.00	0	0.00
U4	0	0.00	0	0.00	0	0.00	0	0.00	3	25.00
U5	0	0.00	1	5.00	0	0.00	0	0.00	0	0.00
U6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U7	0	0.00	1	5.00	0	0.00	0	0.00	1	8.33
U8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
V	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
W	0	0.00	0	0.00	1	5.26	0	0.00	0	0.00
X2	0	0.00	0	0.00	2	10.53	0	0.00	0	0.00
X4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Y	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00

	Syria		Turkey		Yemen		Evenki		Mansi	
	N	%	N	%	N	%	N	%	N	%
Z	0	0.00	0	0.00	0	0.00	1	5.26	0	0.00
	Nganasan		Yakut		Altaian Kazakh		Altaian Kizhi		Buryat	
	N	%	N	%	N	%	N	%	N	%
Haplo-group	12	100.00	11	100.00	13	100.00	20	100.00	20	100.00
A	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
B	0	0.00	1	9.09	0	0.00	3	15.00	7	35.00
C	5	41.67	4	36.36	0	0.00	10	50.00	5	25.00
CZ	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D4	3	25.00	1	9.09	1	7.69	3	15.00	3	15.00
D5	0	0.00	1	9.09	0	0.00	0	0.00	0	0.00
D6	1	8.33	0	0.00	0	0.00	0	0.00	0	0.00
E	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
F	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
G	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
H	0	0.00	0	0.00	7	53.85	0	0.00	0	0.00
HV	0	0.00	0	0.00	1	7.69	0	0.00	0	0.00
I	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
J	0	0.00	2	18.18	0	0.00	0	0.00	0	0.00
JT	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
K	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L3	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M	0	0.00	0	0.00	0	0.00	2	10.00	2	10.00
M7	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M9	0	0.00	0	0.00	1	7.69	0	0.00	1	5.00
N	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N9	0	0.00	0	0.00	0	0.00	0	0.00	2	10.00
P	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00

	Nganasan		Yakut		Altaian Kazakh		Altaian Kizhi		Buryat	
	N	%	N	%	N	%	N	%	N	%
R	0	0.00	0	0.00	0	0.00	1	5.00	0	0.00
R0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
T	0	0.00	1	9.09	0	0.00	0	0.00	0	0.00
U1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U2	0	0.00	0	0.00	1	7.69	0	0.00	0	0.00
U3	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U4	2	16.67	0	0.00	2	15.38	0	0.00	0	0.00
U5	0	0.00	1	9.09	0	0.00	0	0.00	0	0.00
U6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U7	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
V	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
W	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
X2	0	0.00	0	0.00	0	0.00	1	5.00	0	0.00
X4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Y	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Z	1	8.33	0	0.00	0	0.00	0	0.00	0	0.00
	Ket		**Khamnigan**		**Shor**		**Teleut**		**Tofalar**	
	N	%	N	%	N	%	N	%	N	%
Haplo-group	4	100.00	20	100.00	12	100.00	8	100.00	4	100.00
A	1	25.00	0	0.00	0	0.00	0	0.00	0	0.00
B	0	0.00	6	30.00	1	8.33	0	0.00	2	50.00
C	0	0.00	6	30.00	4	33.33	4	50.00	1	25.00
CZ	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D4	0	0.00	6	30.00	1	8.33	0	0.00	0	0.00
D5	0	0.00	0	0.00	1	8.33	0	0.00	0	0.00
D6	1	25.00	0	0.00	0	0.00	0	0.00	0	0.00
E	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
F	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
G	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
H	0	0.00	0	0.00	3	25.00	0	0.00	0	0.00
HV	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
I	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00

	Ket		Khamnigan		Shor		Teleut		Tofalar	
	N	%	N	%	N	%	N	%	N	%
J	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
JT	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
K	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L3	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M	0	0.00	0	0.00	1	8.33	1	12.50	0	0.00
M7	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M9	0	0.00	1	5.00	0	0.00	0	0.00	0	0.00
N	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N2	1	25.00	0	0.00	0	0.00	0	0.00	0	0.00
N9	0	0.00	1	5.00	0	0.00	0	0.00	0	0.00
P	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
T	0	0.00	0	0.00	0	0.00	1	12.50	0	0.00
U1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U3	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U4	0	0.00	0	0.00	1	8.33	1	12.50	0	0.00
U5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U7	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
V	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
W	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
X2	0	0.00	0	0.00	0	0.00	1	12.50	0	0.00
X4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Y	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Z	1	25.00	0	0.00	0	0.00	0	0.00	1	25.00

	Tuvinian		Uyghur		Chukchi		Even		Koryak	
	N	%	N	%	N	%	N	%	N	%
Haplo-group	17	100.00	2	100.00	20	100.00	13	100.00	19	100.00
A	0	0.00	0	0.00	12	60.00	0	0.00	1	5.26
B	1	5.88	0	0.00	0	0.00	0	0.00	0	0.00
C	0	0.00	1	50.00	2	10.00	4	30.77	8	42.11
CZ	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D4	7	41.18	0	0.00	4	20.00	5	38.46	0	0.00
D5	1	5.88	0	0.00	0	0.00	0	0.00	0	0.00
D6	2	11.76	0	0.00	0	0.00	2	15.38	0	0.00
E	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
F	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
G	1	5.88	0	0.00	2	10.00	1	7.69	5	26.32
H	2	11.76	0	0.00	0	0.00	0	0.00	0	0.00
HV	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
I	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
J	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
JT	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
K	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L3	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M	0	0.00	1	50.00	0	0.00	0	0.00	1	5.26
M7	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M9	1	5.88	0	0.00	0	0.00	0	0.00	0	0.00
N	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N9	1	5.88	0	0.00	0	0.00	0	0.00	0	0.00
P	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
T	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00

	Tuvinian		Uyghur		Chukchi		Even		Koryak	
	N	%	N	%	N	%	N	%	N	%
U1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U3	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U4	1	5.88	0	0.00	0	0.00	0	0.00	0	0.00
U5	0	0.00	0	0.00	0	0.00	0	0.00	1	5.26
U6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U7	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
V	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
W	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
X2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
X4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Y	0	0.00	0	0.00	0	0.00	1	7.69	2	10.53
Z	0	0.00	0	0.00	0	0.00	0	0.00	1	5.26
	Negidal		Nivkhi		Udegey		Ulchi		Yukaghir	
	N	%	N		N	%	N	%	N	%
Haplo-group	6	100.00	20	100.00	20	100.00	14	100.00	20	100.00
A	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
B	1	16.67	0	0.00	0	0.00	0	0.00	0	0.00
C	0	0.00	0	0.00	7	35.00	2	14.29	9	45.00
CZ	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
D4	4	66.67	4	20.00	0	0.00	2	14.29	5	25.00
D5	0	0.00	0	0.00	0	0.00	0	0.00	2	10.00
D6	0	0.00	0	0.00	0	0.00	2	14.29	0	0.00
E	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
F	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
G	0	0.00	1	5.00	0	0.00	0	0.00	0	0.00
H	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
HV	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
I	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
J	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
JT	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
K	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00

	Negidal		Nivkhi		Udegey		Ulchi		Yukaghir	
	N	%	N		N	%	N	%	N	%
L1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L3	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M7	0	0.00	0	0.00	4	20.00	0	0.00	0	0.00
M8	0	0.00	0	0.00	3	15.00	1	7.14	0	0.00
M9	0	0.00	0	0.00	2	10.00	0	0.00	0	0.00
N	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N9	0	0.00	0	0.00	2	10.00	1	7.14	0	0.00
P	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
T	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U3	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U7	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
V	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
W	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
X2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
X4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Y	1	16.67	15	75.00	2	10.00	5	35.71	0	0.00
Z	0	0.00	0	0.00	0	0.00	1	7.14	4	20.00

	India		Nepal		Afghanistan		Pakistan		Tibet	
	N	%	N	%	N	%	N	%	N	%
Haplo-group	20	100.00	20	100.00	98	100.00	5	100.00	20	100.00
A	0	0.00	0	0.00	3	3.06	0	0.00	4	20.00
B	0	0.00	0	0.00	1	1.02	0	0.00	1	5.00
C	0	0.00	0	0.00	2	2.04	0	0.00	1	5.00
CZ	0	0.00	0	0.00	2	2.04	0	0.00	0	0.00
D4	17	85.00	0	0.00	2	2.04	0	0.00	3	15.00
D5	3	15.00	0	0.00	0	0.00	0	0.00	1	5.00
D6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
E	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
F	0	0.00	1	5.00	0	0.00	0	0.00	2	10.00
G	0	0.00	0	0.00	2	2.04	0	0.00	3	15.00
H	0	0.00	0	0.00	21	21.43	0	0.00	0	0.00
HV	0	0.00	0	0.00	1	1.02	0	0.00	0	0.00
I	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
J	0	0.00	0	0.00	1	1.02	0	0.00	0	0.00
JT	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
K	0	0.00	0	0.00	25	25.51	0	0.00	0	0.00
L0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L1	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L3	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
L5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M	0	0.00	16	80.00	6	6.12	0	0.00	3	15.00
M7	0	0.00	0	0.00	2	2.04	0	0.00	0	0.00
M8	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
M9	0	0.00	0	0.00	0	0.00	0	0.00	2	10.00
N	0	0.00	0	0.00	1	1.02	0	0.00	0	0.00
N1	0	0.00	0	0.00	1	1.02	0	0.00	0	0.00
N2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
N9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
P	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R	0	0.00	1	5.00	0	0.00	0	0.00	0	0.00
R0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
R9	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
T	0	0.00	2	10.00	5	5.10	0	0.00	0	0.00

	India		Nepal		Afghanistan		Pakistan		Tibet	
	N	**%**	**N**	**%**	**N**	**%**	**N**	**%**	**N**	**%**
U1	0	0.00	0	0.00	4	4.08	0	0.00	0	0.00
U2	0	0.00	0	0.00	4	4.08	3	60.00	0	0.00
U3	0	0.00	0	0.00	4	4.08	0	0.00	0	0.00
U4	0	0.00	0	0.00	5	5.10	0	0.00	0	0.00
U5	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U6	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
U7	0	0.00	0	0.00	4	4.08	1	20.00	0	0.00
U8	0	0.00	0	0.00	2	2.04	0	0.00	0	0.00
U9	0	0.00	0	0.00	0	0.00	1	20.00	0	0.00
V	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
W	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
X2	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
X4	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Y	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Z	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00